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January 5, 2006, 19:12:00; Search time 2902 Seconds (without alignments) 10479.410 Million cell updates/sec
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Copyright (c) 1993 - 2006 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	M19262 Rat clathri	AX401731 Sequence	AX827493 Sequence	M15883 Rat clathri	BT007028 Homo sapi	CR536577 Homo sapi	AY889907 Synthetic	AY892384 Synthetic	AY892385 Synthetic	BT007759 Synthetic	M20470 Human lymph	BC006457 Homo sapi	BC006332 Homo sapi	BC070404 Mus muscu	X04853 Bos taurus	M20469 Human brain	X04852 Bos taurus	CQ729113 Sequence
SUMMARIES	, er	RATCBR3	AX401731	AX827493	RATCBR2	BT007028	CR536577	AY889907	AY892384	AY892385	BT007759	HUMLCTHB	BC006457	BC006332	BC070404	BTLCBRL	HUMBCTHB	BTLCBRB	CQ729113
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4	Query Match	100.0	88.0	88.0	88.0	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	82.7	80.3	72.5	68.3	60.7
	Score	535	471	471	471	451.8	451.8	451.8	451.8	451.8	451.8	451.8	451.8	451.8	442.2	429.4	387.8	365.4	325
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Molecular toxicology modeling
Patent: WO 210453-A 1407 07-FEB-2002;
Gene Logic, Inc. (US)
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
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/mol_type="unassigned DNA"
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Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
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AX827493
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Rattus norvegicus
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Best Local Similarity 90.8%;
Matches 535; Conservative 0
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brovoze 636 bp mRNA linear PRI 13-MAY-2003
Homo sapiens clathrin, light polypeptide (Lcb) mRNA, complete cds.
Brooroze
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1 (bases 1 to 636)
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Elsenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 636)
Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y.,
GAPAASQVASAQPGLASGGGSEDMGTTVNGDVFQEANGPADGYAAIAQADRLTQEPES
IRKWREBGKKRLQELDAASKVTEQEWREKAKKDLEEWNQRQSEQVEKNKINNRIADKA
FYQQPDADTIGYVASEEAFVKESKEETPGTEWEKVAQLCDFNPKSSKQCKDVSRLRSV
LMSLKQTPLSR"
                                                                                                                                                                                                                                TCGGGGCACCTGCCGCCAGCCAGGTGGCCTCTGCGCAGCCCGGACTCGCGAGCGGGGTG 120
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                  CCGATGCCTACGCTGCGATTGCCCAGGCGGACAGGTTGACTCAGGAGCCTGAGAGCATCC
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                                                                                                                                                                                  CGGCCGCCTTCCTGGCCCCAGCAGAGAGCGAGATTGCTGGCATCGAGAATGACTCGGGTT
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                                                                                                 Length 982,
                                                                                                 Score 471; DB 9; Length 98 Pred. No. 8.8e-97; 0; Mismatches 0; Indels
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                                                                      bp upstream of Aval site.
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                                                                                                     88.0%;
90.8%;
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Homo sapiens (human)
                                                                                                                       Best Local Similarity 90.8
Matches 535; Conservative
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Alses:1 GI:203358
Alses:1 GI:203358
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buzrchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
1 (bases 1 to 982)
Mirinahausen, T., Scarmato, P., Harrison, S.C., Monroe, J.J., Chow, E.P., Mattaliano, R.J., Ramachandran, K.L., Smart, J.E., Ahn, A.H. and
Brosius, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein id="AAA40890.1"
/db xref="G1:203359"
/translation="MAEDFGFFSSSESGAPEAAEEDPAAAFLAQQESEIAGIENDSGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROD 27-APR-1993
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Draft entry and computer-readable sequence for [1] kindly provided by T.Kirchhausen, 05-05T-1987.

Location/Qualifiers
                                                                                                                         240
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                                                                             GTTCGGAGGACTACAGTCAATGGAGATGTTTTCAGGAGGTAACGGCCTG
                                                                                                                                               CCGATGGCTACGCTGCGGATTGCCCAGGCGGACAGGTTGACTCAGGAGCCTGAGAGCATCC
                                                                                                                                                                                       GCAAGTGGAGAGAGGAGAGAAAAAGGCTGCAGGAGTTGGATGCTGCCTCGAAGGTGA
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                                                                                                                         CCGATGGCTACGCTGCGATTGCCCCAGGCGGACAGGTTGACTCAGGAGCCTGAGAGCATCC
                                                                                                                                                                                                                                                        CCGAACAGGAGTGGCGGGAGAAGGCCCAAAAAAGACCTGGAGGAGTGGAACCAGCGCCAAA
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Rat clathrin light chain (LCB2) mRNA, complete cdв.
M15883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="LCB2 mRNA"
29. .718
/note="clathryn light chain
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638

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394

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CR536577 636 bp mRNA linear PRI 17-APR-2005 Homo sapiens full open reading frame CDNA clone RZPDo834B0322D for gene CLTB, clathrin, light polypeptide (Lcb); complete cds, incl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RZPD; KZPDO834B032ZD, ORFNO 3192
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDO834B032ZD RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This CDS has been cloned incl. stopcodon.

The CDS has been inserted into pDONR201 via a BP Clonase(TM)

reaction. Additional sequence has been added in front of the start
codon: att. AAAAAA GCA GGC TCC ACC (ATG).

The stopcodon is followed by the 3' att site:

(stop)GACCCAGCTTTCTT. att Compared to the reference sequence
NM 001834 ($132483393) we found AA exchange(s) at position (first
Clone distribution: http://www.rzpd.de/products/orfclones/.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryogista, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi, Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Mammalia; Homo.

1 (bases 1 to 636)
Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S., Korth, B., Zuo, D., Hu, Y. and Labert, K., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and Labert, J.

Cloning of human full open reading frames in Gateway (TM) system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available from R2PD; contact R2DD (contact R2DD (customer.service@rzpd.de) for further information. This CDS clone is a part of a collection of human full ORF clones jointly established and verified by the Harvard Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lallack, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S., Natlack, P., Ebert, L., Mkoundinya, M., Schick, M., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J. Direct Submission Submission Submitted (23-UNN-2004) RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
www.rzpd.de
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/lab_host="DH10B"
605
551 ACCCCAAGAGCAGCAAGCAGTGCAAAGATGTGTCCCGCCTGCGCTCGGTGCTCAT
                                                                                                                                                                                                                                                                                 CR536577.1 GI:49168637
Full ORF shuttle clone, Gateway(TM), complete cds.
Homo sapiens (human)
Homo sapiens
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/mol_type="mRNA"
/db xref="RZPD:RZPDo834B0322D"
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/clone="RZPDo834B0322D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry vector (pDONR201)
Unpublished
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                                                                             Circle, Palo Alto, CA 94303, USA

This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
expression clones generated by BD Biosciences Clontech and the
larvard Institute of Proteomics. Bach CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Fusion (TM)
cloning system between the Sall school and Hindill sites of the pDNR-DUAL
vector. Additional sequences in the clone: 'ACC' after Sall site
and before 'ATG' to provide Kozak consensus sequence; 'GG' after
last codon and before Hindill site to maintain reading frame.
Clone distribution: http://bioinfo.clontech.com/orfclones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/product="clathrin, light polypeptide (Lcb)"
/protein_id="AAP35675.1"
/db_xref="Gl:30582895"
/translation="MADDFGFFSSSESGAPEAAEEDPAAFLAQQESEIAGIENDEGF
GAPAGSHAAPAQPGPTSGAGSEDMGTTVNGDVFQEANGPADGYAIAQADRLTQEPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRKWREEQRKRLQELDAASKVTEQEWREKAKKDLEEWNQRQSEQVEKNKINNRASEEA
FVKESKEETPGTEWEKVAQLCDFNPKSSKQCKDVSRLRSVLMSLKQTPLSR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTCGGAGGACATGGGGACTACAGTCAATGGAGATGTTTTTCAGGAGGCTAACGGGCCTG 180
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  Phelan,M. and Farmer,A.
Direct Submission
Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 Bast Meadow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="GH00332X1.0"
/clone lib="BD Creator(TM) CDS Library derived from MGC
collection"
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Pred. No. 2e-92;
0; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH5alpha Tl resistant"
/note="Vector: pDNR-Dual"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db xref="taxon:9606"
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Williamson, J. and LaBaer, J.
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Synthetic construct Homo sapiens clone FLH025393.01X clathrin light
polypeptide (CLTB) mRNA, complete cds.
/protein_id="CAG38814.1"
/db_xref="G1:49168638"
/db_xref="G0A:P03497"
/db_xref="G0A:P034
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Human ORF Project.

synthetic construct
synthetic construct
synthetic construct
synthetic sequences, artificial sequences.

1 (bases 1 to 636)
Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
Williamson, J. and Labaer, J.

Cloning of human full-length CDS in Creator (TM) recombinational
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Direct Submission
Submitted (04-JAM-2005) Biological Chemistry and Molecular
Submitted (04-JAM-2005) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned with normalized stop-codon. The CDS
This Der clone has been cloned with normalized stop-codon. The CDS
has been directionally cloned using BD In-Pusion(TM) cloning system
between the Sall and HindIII sites of the pDNR-Dual vector.
Additional sequences in the clone: "ACC" after Sall site and
before 'ATG' to provide Kozak consensus sequence. Each clone is
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon start=1
/transT_table=11
/product="clathrin light polypeptide"
/product="clathrin light polypeptide"
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/db_xref="G1:60656269"
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IRKWREEGNKRLQELDAASKVTEGSWREKALKGLEEWNQRQSEQVERNINNBASSER
FVKESKEETPGTEWEKVAQLCDFNPKSSKQCKDVSRLRSVLMSLKQTPLSR"
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/note="derived from MGC template"
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llarity 90.3%; Pred. No. 2e-92;
Conservative 0; Mismatches 52; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="synthetic construct"
/mol_type="mRNA"
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/clone="FLH025393.01X"
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/gene="CLTB"
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/gene="CLTB"
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TCGGGGCACCTGCCGCCAGCCAGGTGGCCTCTGCGCAGCCCGGACTCGCGAGCGGGGTG
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/mol_type="mRNA"
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SOURCE
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                                                                                                                                                                Synthetic construct Homo sapiens clone FLH025388.01L clathrin light PAR82388.01L clathrin light AX892384
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/protein id="AAX29301.1"
/db xref="G1:60653213"
/db x
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                                                                                                                                                                                                                                                                                                                 AY892384.1 GI:60653212

Human ORF project.

Human ORF project.

Hyperic construct

Synthetic construct

other sequences; artificial sequences.

1 (bases 1 to 636)

Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and Labaer, J.

Cloning of human full-length CDS in Creator (TM) recombinational
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Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
Williamson, J. and Labaer, J.
Direct Submission
535
                           ACCCCAAGAGCAGCAAGCAGTGCAAAGATGTGTCCCGGCCTGCGCTCGTGCTCAT 605
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/note="derived from MGC template"
ACCCTAAGAGCAGCAAGCAATGTAAAGACGTGTCCCGCCTGCGCTCGGTGCTCAT
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Pred. No. 2e-92;
0; Mismatches 52; Indels
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/mol_type="mkNA"
/db_xref="taxon:32630"
/clone="FLH025388.01L"
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/transl_table=11
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/gene="CLTB"
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Best Local Similarity 90.3%;
Matches 483; Conservative
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AL Unpublished

Nector system

Nector system

Lupublished

CB (bases 1 to 636)

Rines,L., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F., Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E., Williamson,J. and LaBaer,J.

Milliamson,J. Taycher,E.,

Milliamson,J. and LaBaer,J.

Milliamson,J. Taycher,E.,

Milliamson,J. and LaBaer,J.

Milliamson,J. Taycher,E.,

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Synthetic construct Homo sapiens clone FLH025389.01L clathrin light
POlypeptide (CLTB) mRNA, partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 GCAAGTGGCGAGGAGGAAACGGCTGCAAGAGCTGGTGGTGCTGCATCTTAAGGTCA 370
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Human ORF project.

Bynthetic construct

synthetic construct

synthetic construct

other sequences; artificial sequences.

1 (bases 1 to 636)

Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,

Williamson, J. and Labacr, J.

Cloning of human full-length CDS in Creator (TM) recombinational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGAACAAGTAGAAGAAGAACAAGATCAACAACCGGGCATCCGAGGAGGCTTTCGTGAAGG
251 CTGATGGCTACGCAGCCATTGCCCAGGCTGACAGGTGACCCCAGGAGCCTGAGAGCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 GTGAACAGGTTGAGAAGAACAAGATCAACAACAGGGCATCGGAAGAGGCTTTTGTGAAAG
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                                                                                                                                                                                                                                       <u>errcraagacargegacacacacacrargaargaargrarrrcaggaggacaacgarccra</u>
                                                                                                                                                                                                                                                                                                                                      CCGATGGCTACGCTGCGATTGCCCAGGCGGACAGGTTGACTCAGGAGCCTGAGAGCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAAGTGGAGAGGAGGAGCAGAAGAAAGGCTGCAGGAGTTGGATGCTGCCTCGAAGGTGA
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Unpublished

2 (bases 1 to 636)

Stalnine, N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
Direct Submission

Lorect Submission

Lorect Submission

Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
Circle, Palo Alto, CA 94303, USA

This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Pusion(TM)
cloning system between the Sall and Hindill sites of the pDNR-DUAL
vector. Additional sequences in the clone: 'ACC' after Sall site
and before Hindill site to maintain reading frame.
Clone distribution: http://bioinfo.clontech.com/orfclones.

Location/Qualifiers

I. .636

Location/Gualifiers

Location/Gualifiers

Location/Gualifiers

Location and before Hindill site to maintain reading frame.

Location/Gualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MADDFGFFSSSESGAPEAAEEDPAAFLAQOESEIAGIENDEGF
GAPAGSHAAPAQPGPTSGAGSEDMGTTVNGDVFQEANGPADGYAAIAQADRLTGEPES
IRKWREEGRKRLQELDAASKVTEQEWREKAKKDLEEWNQRQSEQVEKNKINNRASEEA
FVKESKEETPGTEWEKVAQLCDFNPKSSKQCKDVSRLRSVLMSLKGTPLSRL"
Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Bisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.
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/protein_id="AAP36427.1"
/db_xref="GI:30584357"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="BD Creator(TM) CDS Library derived from MGC collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CIGATGGCTACGCAGCCATGCCCAGGCTGACAGCTGACCCAGGAGCCTGAGAGCATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTCGGAGGACTAGGGACTACAGTCAATGGAGATGTGTTTCAGGAGGCTAACGGGCCTG
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Pred. No. 2e-92;
0; Mismatches 52; Indels 0;
                                                       Cloning of human full-length CDSs in BD Creator (TM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       resistant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="Mutations: 635:Stop->Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="synthetic construct"
|mol_type="mRNA"
|db_xref="taxon:3260"
|clone="GH0033211.0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.4%; SCor. 90.3%; Pred. No. ze. ... 0; Mismatches ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH5alpha T1 re:
/note="Vector: pDNR-Dual"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
'transl_table=11
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Best Local S
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                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                TITLE
JOURNAL
         AUTHORS
                                                                                                       JOURNAL
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                                                                                                                                                                                                                                                                           /trainiation="Maddegepssesgapeaaeedpaaaflaqqesbilagiendege
papagshapapeppersqagsemqettyngdydegangepadayaalaqbablingebes
irkwreecqrkqlqeldaaskytegerrekakkoleennqrqsesqyeknkinnraseea
fykeskeetpotewekvaqlcdpfnpksskqckdvsrlrsvlmslkqtplsrl"
                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCGGGGCACCTGCCAGCCAGGCGAGCCTCTGCGCAGCCCGGACTCGCGAGCGGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGAACAGGAGTGGCGGGAGAAGAGCCAAAAAAGACCTGGAGGAGTGGAACCAGCGCCCAAA
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                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 636;
                                                                                                                                                                                                                                                                                                                                                                                            84.4%; Score 451.8; DB 11; Length
90.3%; Pred. No. 2e-92;
ive 0; Mismatches 52; Indels
                                                                                                                                                                                                                  producc="clathrin light polypeptide"
/protein_id="AAX29302.1"
/db_xref="G1:60653215"
                             /clone="PLH025389.01L"
/lab host="Escherichia coli DH5al
/note="derived from MGC template"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 636)
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                                                                                                                                                                                    codon start=1
transI table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BT007759.1 GI:30584356
                                                                                                         /gene="CLTB"
1. .>636
                                                                                                                                                gene="CLTB"
                                                                                                                                                                  note="Lcb
                                                                                                                                                                                                                                                                                                                                                                                                                                      483; Conservative
                                                                                         .>636
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VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
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BT007759
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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VINH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 20, 2003 this sequence version replaced gi:13623458.
On Aug 20, 2003 this sequence version replaced gi:13623458.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLML)
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter, N., Ayelle, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooke, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
MCDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.

It (bases 1 to 1164)

Strausberg RL, Feingold RA, Grouse LH, Derge JG, Klausner RD,
Strausberg RL, Feingold RA, Grouse LH, Derge JG, Klausner RD,
Strausberg RL, Feingold RA, Grouse LH, Derge JG, Klausner RD,
Collins FS, Wagner L, Shemmen CM, Schuler GD, Altschul SF, Zeeberg
B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
Max SI, Wang J, Hsieh F, Diatcherko L, Marusina K, Farmer AA, Rubin
GM, Hong L, Stapleton M, Soates MB, Bonaldo MF, Casavant TL,
Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P,
Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy
SJ, Bosak SA, McEwan PJ, McKernan KJ, Male JA, Gancarene PH,
Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,
Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,
Helton E, Ketteman M, Madan A, Rodriguez S, Sanchez A, Whiting M,
Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,
Smailus DB, Schnerch A, Schein JE, Jones SJ and Marra MA
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                            BCO06332 1164 bp mRNA linear PRI 08-MAR-2005 Homo sapiens clathrin, light polypeptide (Lcb), transcript variant nonbrain, mRNA (cDNA clone MGC:12930 IMAGE:4299637), complete cds.
                                                                                                            480
                                                   619
                                                                                                                                                                  679
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (09-ARR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                             GTGAACAGGTTGAGAAGAACAAGATCAACAGGGCATCGGAAGAGGCTTTTGTGAAAG
                                                                                                               AATCCAAGGAGGAGACCCCAGGCACAGAGTGGGAGAAGGTGGCCCAGCTGTGTGACTTCA
                                                                                                                                                                                                                           human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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Director MGC Project.
Direct Submission
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Homo sapiens
                                                                                                                     421
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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AUTHORS
TITLE
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BC006332
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 32483393.
1. 1099
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fvkeskeetpgterekvqllcdpnpksskqckdvsrlrsvlmslikgtber
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                                                         Andy Chan, Steve S. Chand, Milliam Chow, Alison Cloutier, Ruth Reatherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Rim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabbu, Parvaneh Saeedi, Mr Santos, Angelique Schnerch, Ursula Skalska, Bunes Sanilus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TCGGGGCACCTGCCGCCAGCCAGGTGGCCTCTGCGGAGCCCGGACTCGCGAGCGGGTG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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90.3%; Pred. No. 2.1e-92;
         Cancer Agency, Vancouver, BC, Canada
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130. .765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="synonym: LCB"
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Matches 483; Conserv
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Straubberg, R. Peingold, B. A., Grouse, L. H., Derge, J. G.,
Straubberg, R. L., Peingold, B. A., Grouse, L. H., Derge, J. G.,
Altschul, S. P., Collins, P. S., Wagner, L., Schaefer, C. F., Bhat, N. K.,
Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G. M., Hong, L.,
Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,
Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,
Carninoi, P. Prange, C., Raha, S. S., Loquellano, N. A. Peters, G. J.,
Abramson, R. D., Mullahy, S. J., Bosak, S. A., McKernan, R. J., Mullahy, S. J., Gunaratne, P. H., Richards, S.,
Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,
Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,
Bantfard, G., Blakesley, R. W., Touchman, J. W., Grens, E. D.,
Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
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Mus musculus clathrin, light polypeptide (Lcb), mRNA (cDNA clone MGC: 29250 IMAGE:5699653), complete cds.
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Web site: http://genome.uiowa.edu

Ontact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu

Bonaldo,W.P., Akabogu,I., Bair,J., Bair,J., Crouch,K., Davis,A.,

Pishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,

Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,

Casavant,T., Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-romail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIMIL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
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535
                                                       748
                                              ACCCCAAGAGCAGCAAGCAAAGATGTGTCCCGCCTGCGTCGTCTCT
481 ACCCTAAGAGCAGCAAGCAATGTAAAGACGTGCCCGCCTGCGCTCGGTGCTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (10-MAX-2004) National Institutes of Heal
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
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                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAL Plate: 17 Row: m Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /trānslation="MADDFGFFSSESGAPEAAEEDPAAAFLAQQESEIAGIENDEGF
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FVKESKEETPGTEWEKVAQLCDFNPKSSKQCKDVSRLRSVLMSLKQTPLSR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGGGGCACCTGCCGCCAGCCAGGTGGCCTCTGCGCAGCCCGGACTCGCGAGCGGGGGTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGGGGCACCTGCCGGCAGCCATGCGGCCCCCGGGCCGGGCCCCACGAGTGGGGCTG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTCGGAGGACATGGGGACTACAGTCAATGGAGATGTGTTTCAGGAGGCTAACGGGCCTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGATGGCTACGCTGCGATTGCCCCAGGCGGACAGGTTGACTCCAGGAGCCTGAGAGCATCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAAGTGGAGAGGAGCAGAAAAAAGGCTGCAGGAGTTGGATGCTGCCTCGAAGGTGA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGAACAGGAGTGGCGGGAGAGGCCAAAAAGACCTGGAGGAGTGGAACCAGCGCCCAAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        514 CGGAACAGGAATGGCGGGAGAAGGCCAAGAAGGACCTGGAGGAGTGGAACCAGCGCCAGA 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGAACAGGTTGAGAAGAACAAGATCAACAACAGGGCATCGGAAGAGGCTTTTGTGAAAG 420
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                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="MGC:12930 IMAGE:4299637"
/tissue type="fype, normal, pigmented retinal epithelium"
/clone lib="MHH MGC.43"
/lab_host="DH10B-R"
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/product=="clathrin, light polypeptide, isoform a"
/protein.id="AHH06332.1"
/db_xref="GI:13623459"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.3%; Pred. No. 2.1e-92;
Matches 483; Conservative 0; Mismatches 52; Indels 0;
Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="synonym: LCB"
/db xref="GeneID:1212"
/db_xref="MIM:118970"
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/db_xref="MIM:118970"
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IRKWREBQKKRLQELDAASKVTEQEWREKAKKDLEEWNQRQSEQVEKNKINNRIADKA
FYQQPDADTIGYVASEBAFVKESKEETPGTEWEKVAQLCDFNPKSSKQCKDVSRLRSV
LMSLKQTPLSR"
                                                                                                                                                                         translation="MAEDFGFFSSSESGAPEAAEEDPAAFLAQQESEIAGIENDFGF"
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                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                   DB 9;
                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                  Score 442.2; DB 9
Pred. No. 3.2e-90;
1; Mismatches 18
   /tissue type="Brain, mouse 15
/clone lib="NHH BMAP_ERO"
/lab host="DH10B"
/note="Vector: pXX-ASC"
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                                                    /gene="Cltb"
/db_xref="GeneID:74325"
/db_xref="MGI:1921575"
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0
                                                                                                 gene="Cltb"
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ilarity 87.8%;
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HINCBRL 1033 bp mRNA linear MAM 28-APR-2004 Bos taurus mRNA for clathrin light chain b (lymphocyte LCb). X04853 Y00265

> LOCUS DEFINITION ACCESSION

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/db_xref="UniProt/Swiss-Prot:P04975"
/translation="MADDFGFFSSESGAPEAAEEDPAAFLAQQESEIAGIENDEGF
AFAAGSGGGALAQPGPAAEMAEATOFANGPADGYAAIAQADRLTGEPESI
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VKESKREFFGTEWEKVAQLCDFNPKSSKQCKDVSRLRSVLMSLKQTFLSR"
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                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 1033)
Jackson, A.P., Seow, H.F., Holmes, N., Drickamer, K. and Parham, P.
Clathrin light chains contain brain-specific insertion sequences
and a region of homology with intermediate filaments
Nature 326 (6109), 154-159 (1987)
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Building, Stanford, Ca 94305,
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/protein_id="CAA28544.1"
/db_xref="GI:514"
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Submitted (12-MAR-1987) Jackson
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Location/Qualifiers
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481 ACCCTAAGAGCAGCAAGCAATGTAAAGACGTGCCCGCCGGCGCTGCTGTT 535

Search completed: January 5, 2006, 20:29:50 Job time : 2906 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003ds:* geneseqn2003cs:* geneseqn2004as:* geneseqn2004bs:*

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SUMMARIES

Abk63500 Rat Beque Adb58810 Toxicity-Adb5821 Toxicity-Adv21848 Rat hepat Adv15728 Renal tox Adv41572 Rat cardi Adv41572 Rat cardi Adv4157 Rat cardi Adv7445 Cyclin-de Adx0744 Cyclin-de Adx0744 Human CDN Adx0744 Human CDN Adx0744 Human CDN Adx0741 Cyclin-de Adx0741 Cyclin-de Adx0741 Cyclin-de Adx0741 Human CDN Adx3491 Human CDN Ach32890 Human CDN Ach32890 Human CON Ach32890 Human CON Ach32890 Human CON Ach30613 Human foe Adpo4090 Human col Adr15112 Rat elect Description ADW21848 ADP72639 ADV41572 ABK83950 ADX 07445 ADX 07447 ABK 34444 ABK 34409 ADB53521 ABT42334 ADQ52771 ADP04090 ADB58810 ACH32890 ACH39643 ACH40125 ADJ62744 Query Match Length DB 982 1051 1051 1051 1134 894 451.8 451.8 387.8 387.8 379.2 364.4 293.8 268.8 213.4 Score 535 471 471 471 471 471 Result ŝ

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## ALIGNMENTS

ADR15112 standard; DNA; 535 BP

ADR15112;

neuroleptic; nootropic; antidepressant; eating disorder; tranquilizer; neuropsychiatric disorder; signature gene; electroconvulsive seizure; BCS; schizophrenia; autism; major depressive disorder; MDD; bipolar affective disorder; BAD; psychotic depression; anxiety disorder; eating disorder; attention deficit hyperactivity disorder; neuropsychlatric drug; gene; SS; rat. Identifying compound to treat neuropsychiatric disorder, by contacting cell with test compound, determining expression of signature genes by cell, comparing expression of signature genes to expression in cell not contacted with compound. Rat electroconvulsive seizure (EC) signature gene segid 145. Charles VD; Young TA, 18-SEP-2002; 2002US-0411718P. 09-DEC-2002; 2002US-0431882P. 18-JUN-2003; 2003US-0479970P. 18-SEP-2003; 2003US-00664705 21-OCT-2004 (first entry) (ALTA/) ALTAR C A. (LAEN/) LAENG P. (YOUN/) YOUNG T A. (CHAR/) CHARLES V D. Altar CA, Laeng P, WPI; 2004-580183/56 Rattus norvegicus. US2004152107-A1 05-AUG-2004. 

The inversion described and the contracting a cell with a test compound, determining the expression of one or more signature genes by the cell, each signature gene comprising an uncleic acid that cell, each signature gene comprising an uncleic acid that the test compound, determining the expression of one or more signature genes by the cell, each signature gene comprising an uncleic acid that chybridises to a nucleic acid chosen from 154 fully defined sequences (S1) of e.g., 4154, 1582, 645, 2622, 2858, 1194 and 1227 base pairs as given in the specification and their complements, and comparing determined expression of one or more signature genes to expression in cell not contacted with test compound. Also described are: selecting (M2) one or more signature genes that are: selecting (M2) one or contacted with test compound. Also described are: selecting an europsychiatric disorder; and a kit (1) for detecting an electroconvulsive seizure (ECS) gene signature, comprising several colloquation and ECS signature genes to treat, ameliorate or prevent colloquation and ECS signature genes to treat, ameliorate or prevent signatures and ECS signature genes to treat, ameliorate or prevent couropsychiatric disorders; as also disclosed. (M1) is useful for identifying a compound to treat a neuropsychiatric disorders is also disclosed. (M1) is useful for identifying compounds for treating neuropsychiatric disorders such as makety disorder. (BAD) and psychotic depression. (M1) is useful for identifying compounds for treating neuropsychiatric disorders such as MDD, who are susceptible to neuropsychiatric disorders such as MDD, and psychotic depression who are susceptible compounds for treating neuropsychiatric disorders such as MDD, and psychotic depression of the compounds for treating neuropsychiatric disorders such as MDD, and pressive and respective effective and respective and respective an ö TCGGGGCACCTGCCGCCAGCCAGGTGGCCTCTGCGCAGCCCCGGACTCGCGAGCGGGGTG 120 TCGGGGCACCTGCCGCCAGCCAGGTGGCCTCTGCGCAGCCCGGACTCGCGAGCGGGGGTG 120 CCGATGGCTACGCTGCGATTGCCCAGGCGGACGTTGACTCAGGAGCCTGAGAGCATCC 240 CCGATGGCTACGCTGCGATTGCCCAGGCGGACAGGTTGACTCAGGAGCCTGAGAGCATCC 240 GCAAGTGGAGAGAGGAGCAGAAAAAGGCTGCAGGAGTTGGATGCTGCTCGAAGGTGA 300 GCAAGTGGAGAGAGGAGAAGAAAAAGGCTGCAGGAGTTGGATGCTGCCTCGAAGGTGA 300 CCGAACAGGAGTGGCGGAGAAAAAAAAAACCTGGAGGAGTGGAACCAGCGCCAAA 360 CCGAACAGGAGTGGCGGGAGAAGGCCAAAAAGACCTGGAGGAGTGGAACCAGCGCCAAA 360 GTGAACAGGTTGAGAAGAACAAGATCAACAAGAGGGCATCGGAAGAGGCCTTTTGTGAAAG 420 GTGAACAGGTTGAGAAGAACAAGATCAACAACAGGGCATCGGAAGAGGCTTTTGTGAAAG 420 AATCCAAGGAGGAGCCCCAGGCACAGAGTGGGAGAAGGTGGCCCAGCTGTGTGACTTCA 480 GTTCGGAGGACATGGGGACTACAGTCAATGGAGATGTGTTTCAGGAGGCTAACGGGCCTG 180 1 CGGCCGCCTTCCTGGCCCAGGAGAGCGAGTTGCTGGCTTCGAGAATGACTCGGGTT 60 The invention describes a method of identifying (M1) a compound to treat CGGCCGCCTTCCTGGCCCAGCAGAGAGCGAGATTGCTGGCATCGAGAATGACTCGGGTT 0; Gaps Query Match
100.0%; Score 535; DB 13; Length 535;
Best Local Similarity 100.0%; Pred. No. 1e-132;
Matches 535; Conservative 0; Mismatches 0; Indels 0 Sequence 535 BP; 138 A; 127 C; 190 G; 80 T; 0 U; 0 Other; Claim 1; SEQ ID NO 145; 186pp; English signature gene 361 421 61 181 301 421 61 121 121 181 241 241 301 361 셤 8 셤 ò 셤 Š

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The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the compounds or the progression of these toxic effects by determining the compound comparing these to gene expression in unexposed tissues or toxin and comparing these to gene expression in unexposed tissues or calls. Also included are methods of predicting at least one toxic effect of a compound or progression in unexposed to the compound or progression in a tissue or call sample exposed to the compound of two or expression in a tissue or call sample exposed to the compound of two or more genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression. The method can also be used to identify an agent which modulates the toxic response and predict callular pathways that a compound modulates in a cell. The methods utilise a set of at least two probes (on a solid support in kit form), where each of the probes comprises a sequence that support in kit form), where each of the probes comprises a sequence that support in why pridises to a gene listed in the specification, a computer system comprising a database containing information identifying the expression level in a tissue or call sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification, and a user interface to view the information used to present information identifying the expression level in a tissue or call of at least one gene listed in the specification. The method is useful for elucidating global changes in gene expression and for identifying toxicity markers in drug screening and toxicity assays. The genes and
                                                                                                                                                                                                                                                                Rat sequence differentially expressed in response to a hepatotoxin #1407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells.
GCGCTCGGTGCTCAT 535
                           ACCCTAAGAGCAGCAAGCAATGTAAAGACGTGTCCCGCCTGCGCTCGGTGCTCAT 535
                                                                                                                                                                                                                                                                                                    Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
differential expression; centrilobular necrosis; steatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elashoff MR;
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2001US-0297457P.
2001US-0298884P.
                                                                                                                                           ABK63500 standard; cDNA; 982
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2001US-0290029P.
2001US-0290645P.
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22-MAY-2001;
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2003WO-US003194

31-JAN-2003;

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gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound or agent. Hepatotoxicity is characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence tag (EST) or cDNA derived from a gene which is differentially expressed in response to a hepatotoxic agent
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                                                                                                                                      Gaps
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drug screening; toxicity assay; ds.
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                                                                                                            Length 982;
                                                                                     Sequence 982 BP; 212 A; 266 C; 315 G; 189 T; 0 U; 0 Other;
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                                                                                                         Query Match

Best Local Similarity 90.8%; Pred. No. 1.5e-115;
Matches 535; Conservative 0; Mismatches 0;
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07-AUG-2003

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The present invention relates to a method for predicting a toxic effect

of a compound. The method comprises preparing a gene expression profile

of a tissue or cell sample exposed to the compound, and comparing the

can expression profile to a database comprising SEQ ID 1-4925, where

differential expression of the gene indicates at least one toxic effect.

The method is useful for predicting at least one toxic effect of a compound, pendicting hepatocoxicity or the progression of a toxic effect of a compound, identifying an agent that modulates the onset or progression of a toxic response, predicting the cellular pathways that a compound modulates in a cell, and identifying an agent that modulates at cases one activity of a protein. The method and compositions of the present invention using a database of genes having liver toxin-induced differential expression, are useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity markers in sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed case toxic int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                            Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to the compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTCGGAGGACATGGGGACTACAGTCAATGGAGATGTGTTTCAGGAGGCTAACGGGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 982 BP; 212 A; 266 C; 315 G; 189 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                        Castle
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Pred. No. 1.5e-115;
0; Mismatches 0;
                                                                                                                                                                                                                                                           ď
                                                                                                                                                                                                                                                        Higgs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 3836; 1156pp; English.
                                                                                                                                                                                                                                                           Johnson K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.0%;
90.8%;
                                                31-JAN-2002; 2002US-00060087.
15-WAR-2002; 2002US-0364045P.
15-WAR-2002; 2002US-0364055P.
30-DEC-2002; 2002US-0436643P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 535; Conservative
                                                                                                                                                                                                                                                           Porter M,
                                                                                                                                                                                                 LOGIC INC
                                                                                                                                                                                                                                                                                                                  WPI; 2003-689530/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                           Mendrick
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CCGAACAGGAGTGGCGGAGAAAAGGCCAAAAAAAGACCTGGAGGAGTGGAACCAGCGCCAAA 360
effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Toxic effect; gene expression profile; renal toxicity; toxicity marker; database; drug screening; toxicity assay; rat; ds.
                                                                                                                                                                                                                                                                                            CGCCCCCTTCCTGGCCCAGCAGAGAGCGAGATTGCTGGCATCGAGATGACTCGGGTT
                                                                                                                                                                                                                                                                                                                                                                  TCGGGGCACCTGCCGCCAGCCAGGTGGCCTCTGCGCAGCCGGACTCGCGAGTCGCGGGGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                GTTCGGAGGACATGGGGACTACAGTCAATGGAGATGTTTTCAGGAGGCTAACGGGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGATGGCTACGCTGCGATTGCCCAGGCGACAGGTTGACTCAGGAGCCTGAGAGATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 GCAAGTGGAGAGGAGCAGAAAAAGGCTGCAGGAGTTGGATGCTGCCTCGAAGGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GCCATCGGAAGACGCTTTGTGAAAGAACCA
                                                                                                                                                                                                 88.0%; Score 471; DB 10; Length 982; 90.8%; Pred. No. 1.5e-115; tive 0; Mismatches 0; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAGCAGCAAGCAATGTAAAGACGTGTCCCGCCTGCGCTCGGTGCTCAT
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                                                                                                                                                                Sequence 982 BP; 212 A; 266 C; 315 G; 189 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGAACAGGTTGAGAAGAACAAGATCAACAACAG------
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                                                                                                                                                                                                                    Local Similarity
nes 535; Conserv
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                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic
                                                                             toxic effect; gene expression profile; hepatotoxicity; diagnostic marker; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
                                                           Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4063
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                                                                                                                                                   AGAGCAGCAAGCAATGTAAAAGACGTGTCCCGCCTGCGCTCGGTCTCAT
                                                                                                                               AGAGCAGCAAGCAATGTAAAGACGTGTCCCGCCTGCGCTCGGTGCTCAT
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2002US-0363534P.
2002US-0370248P.
2002US-0371134P.
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2002US-0371150P.
2002US-0371413P.
2002US-0373601P.
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2002US-0378653P.
2002US-0378665P.
2002US-0394230P.
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2002US-0374139P.
2002US-0378370P.
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2002US-0407688P,
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                                                                                                                                                                                                                                                         ADB53521 standard; DNA; 982
                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-731472/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003065993-A2.
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110-AFR-2002; 2
110-AFR-2002; 2
19-AFR-2002; 2
22-AFR-2002; 2
22-AFR-2002; 2
09-MAY-2002; 2
09-MAY-2002; 2
09-MAY-2002; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-2002;
08-APR-2002;
10-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-SEP-2002;
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Elashoff M;
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                       519
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338

158 120 218 180 278

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Gaps

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300

398

458 394 518 426 578

486 638

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> > mean

458 394 518 426 578 486

300 398

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The invention relates to methods of predicting at least one toxic effect (or toxicity progression or the mechanism of toxicity) of a compound. The methods involve detecting the level of expression of at least one of a set of 680 genes ADW21622-ADW22301 or at least one of a set of 17 genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Predicting toxicity of compounds, useful in development of safe drugs, by measuring the differential expression of specific genes in cells exposed to test compounds.
GTTCGGAGGACATGGGGACTACAGTCAATGGAGATGTGTTTCAGGAGGCTAACGGGCCTG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccarcactracerracearraccaadeaacadarraacraagaaccraagaaccarcc
                                                                                                                                                                                         339 GCAAGTGGAGAGAGAGAGAAGAAAAGGCTGCAGGAGTTGGATGCTGCCTCGAAGGTGA
                                                                                                                                                                                                                                                                     CCGAACAGGAGTGGCGGAGAAGGCCAAAAAAGACCTGGAGGAGTGGAACCAGCGCCAAA
                                                                                                                                                                                                                                                                                                      CCGATGACTACCTGCGATTGCCCACGCGCACAGGTTGACTCAGGAGCCTGAGAGCATCC
                                                                                                                                                          GCAAGTGGAGAGAGGAGAAAAAGGCTGCAGGAGTTGGATGCTGCCTCGAAGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGAGGAGACCCCAGGCACAGAGTGGGAGAAGGTGGCCCCAGCTGTGACTTCAACCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GCCATCGGAAGACCTTTGTGAAAGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAGCAGCAAGCAATGTAAAGACGTGTCCCGCCTGCGCTCGGTGCTCAT 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Toxicology screening; drug screening; gene expression; expression profile; hepatotoxicity; drug-induced; hepatitis; liver disease; gastrointestinal disease; gene; ss.
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17-JUL-2002; 2002EP-00015657.
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GENBANK; M15883.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ή
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Predicting at least one toxic effect of a compound, useful for toxicity modeling, comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression
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2001US-0331805P.
2001US-0336144P.
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2002US-0357843P.
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2001US-0324928P.
2001US-0330462P.
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21-APR-2002; 2002US-0371679P.
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2001US-0303808P.
2001US-0303810P.
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Best Local Similarity
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10-JUL-2001; 2
28-AUG-2001; 2
27-SEP-2001; 2
22-OCT-2001; 2
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21-NOV-2001;
06-DEC-2001;
19-DEC-2001;
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21-FEB-2002;
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15-MAR-2002;
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confidential ADW22362, ADW22414 and ADW22481-ADW22483) in a tissue or cell exposed to the compound, and determining whether the gene is differentially expressed compared with a control tissue or cell.

Differentiall expression of the gene in the presence of the compound is indicative of a toxicity. The toxic effect, of toxicity progression or of a specific mechanism of toxicity. The toxic effect, protein adduct formation or fatty.

CC mechanism of toxicity. The toxic effect is especially hepatoroxicity, particularly hepatotis, liver necrosis, protein adduct formation or fatty.

CC liver. The invention also relates to sets of primers and probes specific or at least two genes selected from ADW21622-ADW22301; solid supports (e.g., DNA chips) and kies containing the probes; and a database containing DNA sequence information and expression information for at least two of the 680 genes from hepatotoxin-exposed tissues. The invention is based on the determination of global changes in gene expression in tissues or cells exposed to known toxins, particularly mediated by various classes of compounds. Such compounds in gene expression can be characteristic of different mechanisms of hepatotoxicity mediated by various classes of compounds. Such compounds which cause an accumulation of fat in the liver; and include direct acting compounds which cause damage to macromolecules, especially proteins and lipids by directly interacting with them, steatotic compounds which cause an accumulation of fat in the liver; and toxicology screening for predicting the toxic effects (especially compounds which represent specifically claimed hepatotoxicity marker genes of rat origin whose expression is altered on exposure to hepatotoxins.

XX Sequences ADW21622-ADW22301 represent specifically or other;
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158 TCGGGGCACCTGCCGCCAGCCAGGTGGCCTCTGCGCAGCCCGGACTCGCGAGCGGGGTG 120 159 TCGGGGCACCTGCCGCCAGCCAGGTGGCCTCTGCGCAGCCCGGACTCGCGAGCGGGGGGGTG 218 180 219 GTTCGGAGGACATGGGGACTACAGTCAATGGAGATGTGTTTCAGGAGGCTAACGGGCCTG 278 240 279 CCGATGGCTACGCTGCGATTGCCCAGGCGGACAGGTTGACTCAGGAGCCTGAGAGACATCC 338 GCAAGTGGAGAGGAGCAGAAGAAAGGCTGCAGGAGTTGGATGCTGCTCGAAGGTGA 300 GCAAGTGGAGAGGAGCAGAAGAAAGGCTGCAGGAGTTGGATGCTGCCTCGAAGGTGA 398 99 CGCCCCTTCCTGCCCCAGCAGAGCGAGATTGCTGGCATCGAGAATGACTCGGGTT GTTCGGAGGACATGGGGACTACAGTCAATGGAGATGTTTTCAGGAGGCTAACGGGCCTG CCGATGGCTACGCTGCGATTGCCCAGGCGGACAGGTTGACTCAGGAGCCTGAGAGCATCC 1 CGGCCGCCTTCCTGGCCCAGCAGAGAGCGAGATTGCTGGCATCGAGAATGACTCGGGGTT Gaps 54; Query Match

88.0%; Score 471; DB 11; Length 982;
Best Local Similarity 90.8%; Pred. No. 1.5e-115;
Matches 535; Conservative 0; Mismatches 0; Indels 54 Sequence 982 BP; 212 A; 266 C; 315 G; 189 T; 0 U; 0 Other; 61 121 181 339 301 241

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The invention relates to a method of predicting (the progression of) a toxic effect of a compound by preparing a gene expression profile of a toxic effect of a compound by preparing a gene expression profile to a database, or detecting the level of gene (s) gene expression in a tissue or cell sample exposed to the compound, where differential gene expression compared to a control indicates a toxic differential gene expression. The method is useful for predicting (the progression of) at least one toxic effect of a compound. The genes are useful as toxicity markers in drug screening and toxicity assays. The progression of) at least one toxic effect of a compound. The genes are useful for predicting the likelihood that a compound or test agent will induce various specific kidney pathologies, such as nephritis, capent will induce various specific kidney pathologies, such as nephritis, capent will induce various specific kidney pathologies, such as nephritis, capent will induce various specific kidney pathologies, such as nephritis, capent will induce various specific capent injury, or focal segmental glomerulosclerosis. The methods are useful for determining the similarity of a toxic response to one or more individual compounds and for predicting or modelling the potential cellular pathways influenced, induced or modelling the progression of renal disease states, for identifying genes that show promise as new drug targets and for screening known and newly designed drugs. This sequence corresponds to a gene marker used in the method of the invention. (Note: The sequence data for this patent did not form the drug target and for screening known and newly designed through the progression, that was obtained in electronic form part of the printed specification, but was obtained in electronic form part of the printed specification, but was obtained in electronic form part of the printed specification, but was obtained electronic form part of the progression of the toxic response of a gene marker used in the form will and Predicting (the progression of) a toxic effect of a compound, for monitoring the progression of renal disease states, comprises preparing a gene expression profile of a kidney tissue or cell sample exposed to the marker; 687 ds; toxic effect; gene expression profile; kidney tissue; differential gene expression; toxicity progression; toxicity drug screening; toxicity assay; kidney pathology; nephritis; kidney necrosis; glomerular injury; tubular injury; focal segmental glomerulosclerosis. 639 AGAGCAGCAAGCAATGTAAAGACGTGTCCCGCCTGCGCTCGGTGCTCAT Higgs B; Castle A, Renal toxin progression gene marker #1228. Claim 11; SEQ ID NO 1228; 266pp; English. Mendrick DL, Porter MW, Johnson KR, Blashoff M; 멂 24-NOV-2003; 2003WO-US037556. 22-NOV-2002; 2002US-00301856. ADP72639 standard; DNA; 982 26-AUG-2004 (first entry) (GENE-) GENE LOGIC INC. WPI; 2004-460771/43. Rattus norvegicus WO2004048598-A2 10-JUN-2004 ADP72639; compound. ADP72639 

Sequence 982 BP; 212 A; 266 C; 315 G; 189 T; 0 U; 0 Other;
Query Match
Best Local Similarity 90.8%; Pred. No. 1.5e-115;
Matches 535; Conservative 0; Mismatches 0; Indels 54; Gaps

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GTTCGGAGGACATGGGGACTACAGTCAATGGAGATGTTTTCAGGAGGCTAACGGGCCTG
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REFSEQ; NM_053835.
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The invention relates to a method of predicting at least one toxic effect of a compound by obtaining a gene expression profile of a tissue or cell sample exposed to the compound and comparing the gene expression profile to a database of toxicity prediction genes which are differentially expressed on exposure to known toxins. The tissue or cell sample is preferably derived from heart tissue, and the predicted toxic effect is cachycardia, myocardial ischemia, and the predicted toxic effect is cachycardia, myocardial ischemia, angula, hyperension, hyperension, dyspnea, cardiogenic shock or other specific heart pathologies. The invention is based on the elucidation of global changes in gene expression in tissues or cells exposed to known toxins, particularly cardiotoxins, and the identification of individual genes (toxicity cardiotoxins, and the identification of individual genes (toxicity of a cardiotoxins, and the identification of individual genes (toxicity of a compound's toxic effects, for predicting the cardiotoxicity of a compound, for identifying an agent that modulates the progression of a toxic response, and for predicting which cellular progression of a toxic response, and for predicting which cellular predicting the toxic effects who hybridization probes specific for toxicity predicting the toxic effects who hybridization probes specific for toxicity predicting the toxic effects (sepecially cardiotoxic marker compounds such as pharmaceutical agents or environmental pollutants. Sequences ADV39135-ADV41830 represent cardiotoxicity marker compounds such as pharmaceutical agents or environmental pollutants. Sequences ADV39135-ADV41830 represent cardiotoxicity marker compounds such as pharmaceutical agents or environmental pollutants. Sequences ADV39135-ADV41830 represent cardiotoxicity marker compounds such as pharmaceutical agents of the sequence data for this patent distoric for meat of the printed specification, but was obtained in electronic form part of the printed specific at least tone cardiotoxian, Predicting a toxic effect of a compound by obtaining a gene expression profile of a tissue or cell sample exposed to the compound and comparing the gene expression profile to a database comprising all of the data given in the specification. Example 1; SEQ ID NO 2438; 520pp; English 

Sequence 982 BP; 212 A; 266 C; 315 G; 189 T; 0 U; 0 Other;

458 518 120 180 338 300 360 426 158 218 278 9 159 TCGGGGCACCTGCCGCCAGCCAGGGGCCTCTGCGCAGCCCGGACTCGCGAGCGGGGGTG GCAAGTGGAGAGAGGAGAAGAAAAGGCTGCAGGAGTTGGATGCTGCCTCGAAGGTGA CCGAACAGGAGTGGCGGGAGAAGAGCCAAAAAAGACCTGGAGGAGTGGAACCAGCGCCCAAA --GGCATCGGAAGAGGCTTTTGTGAAAGAATCCA GTTCGGAGGACATGGGGACTACAGTCAATGGAGATGTCTTTCAGGAGGCTAACGGGCCTG GTTCGGAGGACATGGGACTACAGTCAATGGAGATGTGTTTTCAGGAGGCTAACGGGCCTG CCGATGGCTACGCTGCGATTGCCCCAGGCGGACAGGTTGACTCAGGAGCCTGAGAGCATCC GCAAGTGGAGAGAGCAGAAAAAAGGCTGCAGGAGTTGGATGCTGCCTCGAAGGTGA TCGGGGCACCTGCCGCCAGCCAGCTCTCTGCGCAGCCCGGACTCGCGAGCGGGGGTG 1 CGGCCGCCTTCCTGGCCCAGCAGGAGAGAGATTGCTGGCATCGAGAATGACTCGGGTT Gaps 54; Length 982; Indels GTGAACAGGTTGAGAAGAACAAGATCAACAACAG------88.0%; Score 471; DB 13; 90.8%; Pred. No. 1.5e-115; iive 0; Mismatches 0; Best_Local Similarity 90.8 Matches 535, Conservative 399 66 61 121 219 279 241 339 361 459 181 301 Query Match ઠે 쉽 ò g ઠે g ઠે 셤 ð 셤 ò 셤 ઠે 셤

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The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the modulating GCA or an inflammation (especially chronic) in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a pathogen or sterile inflammatory disease, by detecting the level of expression of the gene is indicative of inflammation; (4) treating c expression of the desease, by detecting the level of expression of the gene is indicative of inflammation; (4) treating c expression of the gene is indicative of inflammation; (4) treating c response in a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an employed. Expression of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(8) from Gs in the tissue. M1 is useful for screening an agent capable of modulating GA preferably in an
                                                                                                              519 AGCCAGATGCTGATACCATTGGCTATGTGGCATCGGAAGAGGCTTTTGTGAAAGAATCCA 578
                                                                           Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; 88; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; tungal infection; persiste inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ANDS; adult respiratory stress syndrome; inflammatory bowel disease; crohm; s disease; ulcerative colitis; periodontal disease;
                                                                                                                                                                                                                            535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA differentially expressed in granulocytic cells #521
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inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection, parasitic infection, protozoal infection, fungal infection and MS is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 451.8; DB 6;
Pred. No. 2.1e-110;
0; Mismatches 52;
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Matches 483; Conservative
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                                                                                                                                                                                                                                                                       The invention relates to an array for screening a patient for resistance to docetaxel comprising complementary nucleic acid probes attached to a solid surface for at least 10 of the nucleic acids chosen from 91 fully defined sequences as given in the specification. The array is useful for screening a patient for resistance to docetaxel. The array is also useful
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                                                                                                                                                                                                     Array useful for screening patient for resistance to docetaxel comprises complementary nucleic acid probes attached to solid surface.
                                                                                                                                                                                                                                                                                                                                           for monitoring a cancer patient receiving docetaxel therapy. The present sequence represents a human cDNA differentially expressed in response to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGAACAGGTTGAGAAGAACAAGATCAACAACAGGGCATCGGAAGAGGCTTTTGTGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                            84.4%; Score 451.8; DB 12; 90.3%; Pred. No. 2.1e-110; iive 0; Mismatches 52;
                                                                                                                                                                                                                                                Claim 21; SEQ ID NO 14; 169pp; English
                                                     16-MAY-2003; 2003US-00439703
                                                                             17-MAY-2002; 2002US-0381141P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 483; Conservative
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                                                                                                         (CHAN/) CHANG J C. (OCON/) O'CONNELL P.
                                                                                                                                                                           WPI; 2004-224389/21
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
US2004018527-A1
                           29-JAN-2004
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                                                                                                                                                   Chang JC,
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This invention describes a novel method of predicting or determining whether a mammal will respond or is responding to an anti-cancer agent that modulates cyclin-dependent kinase (cdk) activity. The method comprises measuring the level of one or more biomarkers selected from comprises measuring the level of one or more biomarkers selected from CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID comprise) is especially preferred). The method of the invention is utilized in a kit for determining or predicting whether comparison is utilized in a kit for determining or predicting whether cutilizing individualized genetic profiles for treating diseases and ciscorders based on patient's response and molecular level, specialized microarrays comprising the biomarkers described, antibodies directed ciscorders and a call culture model to identify biomarkers. The cdk modulator is preferably N-2-(CC against the biomarkers and a call culture model to identify biomarkers. The cdk modulator is preferably N-2-(CC arcaric acid salt, Note: The sequence data for this patent did not form to tartaric acid salt, Note: The sequence data for this patent did not form directly from WIPO at ftp.wipo.int/pub/published_pot_sequences. This comparison.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biomarkers useful for predicting or determining the response of a mammal to a cancer treatment comprising administration of a modulator of cyclin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 Tededeckerecegeckérekrésékereketeketekedecekekekerekerek
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pred. No. 2.1e-110;
0; Mismatches 52; Indels 0;
                                                                                                                                                                                               Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 2011
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                                                                                                                                                                                                                                                           cytostatic; cyclin-dependent kinase; cdk; biomarker; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wong TW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; SEQ ID NO 2010; 141pp; English.
BP.
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ADX07445 standard; DNA; 1051
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Best Local Similarity 90.3
Matches 483, Conservative
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dependent kinase activity
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                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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oxazoly]]methyl]thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-tartaric acid salt. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published pct sequences. This sequence encodes a biomarker used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ss; gene; secreted protein; immune deficiency; viral infection; bacterial infection; fungal infection; autoimmune disorder; burn; theumatoid arthritis; multiple sclerosis; autoimmune thyroiditis; diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour; cosquitation disorder; haemophilia; inflammatory disorder; ulcer; tissue regeneration; wound healing; haematopolesis; myeloid deficiency; lymphoid cell deficiency.
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                                                                                                                                                                                              DB 14; Length 1134;
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                                                                                                                                                 Sequence 1134 BP; 225 A; 338 C; 390 G; 181 T; 0 U; 0 Other;
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                                                                                                                                                                                              Score 387.8; DB 1.
Pred. No. 2.7e-93;
0; Mismatches 52
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Best Local Similarity 82.0'
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     CTGATGGCTACGCAGCCATTGCCCAGGCTGACAGGCTGACCCAGGAGCCTGAGAGCATCC
                                                                             GCAAGTGGAGAGGAGCAGAAGAAAAGGCTGCAGGAGTTGGATGCTGCCTCGAAGGTGA
                                                                                                         GCAAGTGGCGAGAGGAGCAGAAGGAAACGGCTGCAAGAGCTGGATGCTGCATCTAAGGTCA
                                                                                                                                                                          CCGAACAGGAGTGGCGGGAGAAGGCCAAAAAGACCTGGAGGAGTGGAACCAGCGCCAAA
                                                                                                                                                                                                   GTGAACAGGTTGAGAAGAACAAGATCAACAACAGGGCATCGGAAGAGGGCTTTTGTGAAAG
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P-PSDB; ADX07448.
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Pred. No. 1.8e-91;
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                                                                                                                                                                                                                                                 Fechtel K,
                                                                                                            29-MAR-2001; 2001WO-US010295.
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                                                                                                                                                                                                                                                    Clark HF,
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Best Local Similarity
                   WO200177290-A2
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Gulukota K,
                                                                 18-OCT-2001
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The invention relates to 625 polynucleotides which have been derived from a variety of human tissue sources and which encode novel secreted proteins, their complements and sequences that hybridise to them. Also included are a vector comprising the polynucleotide, a host cell transformed with the vector, the proteins encoded by the polynucleotide antibodies that bind to the proteins and identification of modulators of the proteins or the expression of the polynucleotide. The polynucleotide can be used as probes for the identification and isolation of full length cDNA and genomic DNA. The polynucleotides and proteins can also be used as nutritional supplements. The protein is useful in the treatment of various immune deficiencies and disorders such as viral infections, bacterial infections, fungal infections, autoimmune disorders (e.g. 493 355 594 GGAATGGCGGGAGAAGGCCAAGAAGGACCTGGAGGAGTGGAACCAGCGCCAGAGTGAACA 535 475 433 Six hundred and twenty five polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders. Human; ss; gene; secreted protein; immune deficiency; viral infection; bacterial infection; fungal infection; autoimmune disorder; burn; theumacoid arthrittis; multiple sclerosis; autoimmune thyroiditis; diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour; cosquitation disorder; haemophilia; inflammatory disorder; ulcer; tissue regeneration; wound healing; haematopolesis; myeloid deficiency; lymphoid cell deficiency. 474 TGCTGATATCATCGGCTACGTGCCATCCGAGGAGGCTTTCGTGAAGGAATCCAAGGAGGA GACCCCAGGCACAGAGTGGGAAAGGTGGCCCAGCTGTGTGACTTCAACCCTAAGAGCAG -----GGCATCGGAAGAGCTTTTGTGAAAGAATCCAAGGAGGA Resnick RJ; Howes SH, CAAGCAATGTAAAGACGTGTCCCGCCTGCGCTCGTCAT 535 354 CAAGCAGTGCAAAGATGTGTCCCGCCTGCGCTCGGTGGTCTTAT Human cDNA for novel secreted protein, SEQ ID 178. Agostino MJ, Claim 1; Page 118-119; 339pp; English. GGTTGAGAAGAACAAGATCAACAACAG-Fechtel K, ABK34409 standard; cDNA; 907 BP. 29-MAR-2001; 2001WO-US010295. 06-APR-2000; 2000US-0194941P. (first entry) (GEMY ) GENETICS INST INC Wong GG, Clark HP, Fe Gulukota K, Graham JR; WPI; 2002-179323/23. ------WO200177290-A2 Homo sapiens. 08-MAY-2002 18-OCT-2001 494 ( ABK34409; 368 395 434 ABK34409/ ID ABK3

30-JUL-2001; 2001US-00918995 30-JUL-2001; 2001US-00918995

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genome mapping; biodiversity; genetic disorder.
            diabetes) and allergic reactions and conditions (e.g. asthma). They are also useful for treating neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), liver fibrosis, coagulation disorders (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and tumours. They are also useful for tissue regeneration, for wound healing and in the treatment of burns, incisions and ulcers. The proteins are also useful for regulating heamatopoicsis, for treating mysloid or lymphoid cell deficiencies. The present sequence is one of the 625 cDNA
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autoimmune thyroiditis and
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                                                                                                                                                                                                              DB 6; Length 907;
                                                                                                                                                                            Sequence 907 BP; 162 A; 279 C; 257 G; 209 T; 0 U; 0 Other;
                                                                                                                                                                                                                                             53; Indels
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                                                                                                                                                                                                              Score 379.2; DB 6
Pred. No. 4.9e-91;
                                                                                                                                                                                                                                               0; Mismatches
rheumatoid arthritis, multiple sclerosis,
                                                                                                                                               sequences encoding a secreted protein
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81.6%;
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Best Local Similarity
Matches 475; Conserv
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH5081, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polyneptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are asfall in diagnostics as expressed sequence tags (BST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide genesors also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly approach.
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consists of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleos Bukaryota, Eutheria, Eurchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
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1. (bases 1 to 682)
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Rat Genome Project: Generation of a Rat EST (REST) Catalog & Unpublished (1998)
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The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850,
Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                           100.0%; Score 535; DB 1; L 100.0%; Pred. No. 4.6e-121; ive 0; Mismatches 0;
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

I (bases I to 844)
II (bases I to 844)
INH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                           /mol_type="mRNA" [
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/clone="RGIAD81"
/clone="RGIAD81"
/clone="Normalized rat brain, Bento Soares"
/note="Organ: brain; Vector: pT773Pac; Site_1: EcoRI; Site_2: NotI"
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                   contact the ATCC
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                                                                                                                                                                                                                                                                         ; Score 535; DB 1; I; Pred. No. 4.8e-121; 0; Mismatches 0;
Email: nhlee@tigr.org
This clone is available through the ATCC,
tel#703-165-2700 for further information
Seq primer: M13 Reverse.
                                                                                                               gb.
                                                                   Location/Qualifiers

    .682
    /organism="Rattus

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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Located 420, 563-573 (2002)

E (bases 1 to 1577)

E (b
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Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833419E16 product:clathrin, light polypeptide (LCD), full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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Direct Submission
Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
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FANTOM CONSORTIUM. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                                                                                                                             Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 cedececerriceredeceaecadaaadeceaearrecredeareaaareaeceegerr 137
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Pred. No. 6.2e-114;
0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Best Local Similarity 96.6%;
Matches 517; Conservative
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Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
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Sciurognathi; Muroidea; Muridae; Musinae; Mus.

Sciurognathi; Muroidea; Muridae; Musinae; Mus.

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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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Hayashizaki,Y.
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/clone lib="R1KEN full-length enriched mouse cDNA library"
/dev_gtage="0 day neonate"
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Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-rese@gsc.riken.jp, UKL:http://genome.gsc.riken.jp/, Tel:81-45-503-922, Pax:81-45-503-9216)

cDNA 11brary was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
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Location/Qualifiers
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0; Mismatches 18;
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/note="putative"
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Best Local Similarity 96.6%;
Matches 517; Conservative (
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Unpublished (2011)

On Jul 1, 1999 this sequence version replaced gi:5315593.

Contact: Yoshinide Hayashizaki
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Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Exa: 81
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Computational Analysis of Full-Length Mouse cDNAs Compared with
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                                                                                                                           Sciurognathi, Murciolea, Muridae; Gilres; Rodentia; Sciurognathi, Murciolea, Murinae; Mus.

1 (bases 1 to 1026)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kouda, M., Salto, R., Sakai, C., Sakai, C., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogbe, Y., Sauxiki, H., Tagami, M., Tagawa, A., Takahashi, F., RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 GCCGCCTTCCTGGCCCAGCAGAAAGCGAGATTGCTGGCATCGAGAATGACCCGGGTTTC
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Please visit our web site (http://genome.gsc.riken.go.jp/)
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/clone_lib="Mus_musculus_C57BL/6J_11-day_embryo"
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Pred. No. 3e-112;
0; Mismatches 21; Indels
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/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="2700067L17"
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                            Mus musculus (house mouse)
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llarity 96.1%;
Conservative
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGATGGCTACGCTGCGATTGCCCCAGGCGGACAGGTTGACTCAGGAGCCTGAGAGCATCC 240
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                                                                                                                                  clone_lib="RIKEN full-length enriched, 0 day neonate
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ilarity 96.3%; Pred. No. 3.6e-113;
Conservative 0; Mismatches 20.
                                    /tissue_type="head"
/dev stage="0 day neonate"
/lab_host="DH10B"
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AV129358
AV129358.2 GI:16382589
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/note="vector: pSPORT1 (Invitrogen); Site_1: Sal1; Site_2: Not1; Mouse cDNA project by the Laboratory of Genetics.
National Institute on Aging (NIA). Intramural Research Program, NIH (http://lgun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 13 embryos at 8.5-days postcoitum. Double-stranded cDNAs were synthesized with an Oligodfi) primer [Invitrogen:
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                          /clone_lib="NIA Mouse 8.5-dpc Whole Embryo cDNA Library (Long)"
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Pred. No. 5.4e-112;
0; Mismatches 18;
/dev_stage="8.5-days_postcoitum"
/lab_host="DH10B"
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Piao,Y., Ko,N.T., Lin,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
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                                                                                                                                                                     GATGGCTACGCTGCGATTGCCCAGGCGGACAGGTTGACTCAGGAGCCTGAGAGCATCCGC 242
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                                                                                                                                                                                                                                          AAGTGGAGAGAGGAGCAGAAAAAGGCTGCAGGAGTTGGATGCTGCCTCGAAGGTGACC 302
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                                                                                                                                                                                                                                                                                                                GAACAGGAGTGGCGGGAGAAGAGCCAAAAAAGACCTGGAGGAGTGGAACCAGCGCCAAAGT 362
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                                                                                                                                                                                                                                                                                                                                                                                                                     538 GAACAGGTTGAGAAGAACAAGATCAACAACAGGGCATCGGAAGAGGGCTTTTGTGAAAGAA 597
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K0835B11-3 NIA Mouse 8.5-dpc Whole Embryo cDNA Library (Long) Mus musculus cDNA clone NIA:K0835B11 IMAGE:30081718 3', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
                                            238 GGGGCACCTGCCGCCAGCCAGGTGGCCTCTGCGGCAGCCGGCACTCGCGAGCGGGGTTGGT
                                                                                                                                                                                        GATGCGTACGCTGCGGATTGCCCAGGCGGGCACAGGTTGACTCAGGAAGCCCGAGAGCATCCGG
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Acronomism="Mus musculus"
/mol_type="mans"
/mol_type="mans"
/strain="c57BL/6J"
/db_xref="niaEST:K0835B11-3"
/db_xref="taxon:10090"
/clone="N1A:K0835B11 INAGE:30081718"
/tissue type="whole embryo including extraembryonic tissues at 8.5-days postcoitum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdnaedgeun:grc.nia.nih.gov
Plate: K0835 row: B column: 11
Seg primer: -21M13 Forward
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/note="Vector: pSPORT1 (Invitrogen); Site 1: Sal1; Site_2: Not1; Mouse cDNA project by the Laboratory of Genetics, National Institute on Adding (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 153-1558 (2001). [PMID: 11544199]). Total RNAS were extracted from a pool of 13 embryos at 8:5-days postcoitum. Double-extranded cDNAS were synthesized with an Oligo(dT) primer [Invitrogen: 5-Gays postcoitum. Double-extranded cDNAS were synthesized with an Oligo(dT) primer [Invitrogen: 5-Gays postrogrammer [Invitrogen: 5-Gays postrogrammer [Invitrogen: 5-Gays postrogrammer [Invitrogen: 5-Gays portion of 10 of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAS were ligated to Long-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the conna were purified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAS were digested with Sal1 and NotI enzymes and cloned into Sal1/NotI site of pSPORTI plasmid vector. The DHADB & coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."
                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 612)
Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                 Mus musculus (house mouse)
Mus musculus
Mus musculus
Mus reserva (Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Musinae; Mus
KO855H11-3 NIA Mouse 8.5-dpc Whole Embryo cDNA Library (Long) Mus
musculus cDNA clone NIA:K0855H11 IMAGE:30083710 3', mRNA sequence
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/dev stage="8.5-days postcoitum"
/lab_host="DH10B"
/clone lib="NIA Mouse 8.5-dpc Whole Embryo cDNA Library (Long)"
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National Institute on Aging/National Institutes of Health
313 Cassell Drive, Sulte 4000, Baltimore, MD 21224-6820, USA
Email: cdnal@lgsun.grc.nia.nih.gov
Plate: K0855 row: H column: 11
Seg primer: -21M13 Forward
High quality sequence stop: 612
POLYAPYES
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/db_xref="taxon:10090"
/clone="NIA:K0855H11 IMAGE:30083710"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 11 (9), 1553-1558 (2001)
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/strain="C57BL/6J"
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                                                                       CK344230
CK344230.1 GI:40299843
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Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements Seg primer: MI3 Forward
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UI-M-CGOp-bre-h-11-0-UI.81 NIH BMAP_Ret4_S2 Mus musculus CDNA clone
UI-M-CGOp-bre-h-11-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                             GTTGAGAAGAACAAGATCAACAACAGGCATCGGAAGAGGGCTTTTGTGAAAGAATCCAAG 428
                                                                                                                                                                                                                                                                                                                                                                                                       361 GITGAGAAGAACAAGATCAACAACAGGGCATCGGAAGAGGCTTTTGTGAAAGAATCCAAG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
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                                                                                                                                                             181 TACGCTGCGATTGCCCAGGCGGACAGGTTGACTCAGGAGCCCGAGAGCATCCGGAAGTGG 240
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
61 CTGCCGCCAGCCAGGTGGCCTCTGCGAGCCGGGACTCGCGAGCGGGGCTGGTTCAGAG
                                                                             AGAGAGGAGCAGAAGAAAAGGCTGCAGGAGTTGGATGCTGCCTCGAAGGTGACCAG
                                                       GACATGGGGACTACAGTCAATGGAGATGTGTTTCAGGAGGCTAACGGGCCTGCCGATGGC
                                                                                                                                189 TACGCTGCGATTGCCCCAGGCGGACAGGTTGACTCAGGAGCCTGAGAGCATCCGCAAGTGG
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCAGCAAGCAATGTAAAGACGTGTCCCGCCTGCGCTCGTCTCAT 535
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Mus musculus
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Fax: 301 443 9890
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/mol_type="mRNA" /strain="C57BL/6J"

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/tissue_type="tumor, gross tissue"
/dev stage="5 months"
/dev stage="5 months"
/lab_lost="bH108"
/clone_lib="NCI CGAP Mam4"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furth,
NHR Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354 AAGAACAAGATCAACAACAGGGCATCGGAAGAGGCTTTTTGTGAAAGAATCCAAGGAGGAG
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                                                                             CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1883 row: a column: 23
High quality sequence stop: 718.
Location/Qualifiers
                                              Priscilla
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       Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D.,
Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.7%; Score 490.6; DB 3;
llarity 96.4%; Pred. No. 4.2e-110;
Conservative 0; Mismatches 19;
                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol type="mRNA"
/strain="NMRI"
/db xref="taxon:10090"
/clone="IMAGE:5347486"
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       /AZTER=TAXANI:1009.
/AZTER=TAXANI:1009.
/lab_host="DH10B (Life Technologies)"
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/note="Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; The NIH BWAP Ret4 S2 library is a subtracted library.
ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu. The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine
TAG_SEQ=None found"
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Pred. No. 9.2e-111;
0; Mismatches 19;
xref="taxon:10090"
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BI659300
BI659300.1 GI:15573536
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Matches 515; Conservative
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Sclurognath, Muroldea; Muroldea; Muridae; Mus. Sclurognath, Muroldea; Muroldea; Muroldea; Muroldea; Muroldea; Muroldea; Muroldea; Sclurognath, Mikaido,I., Osacho,N., Kasukawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Kiyosawa,H., Yaqi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Ouackenbush,J., Schriffl,L.M., Kanapin,A., Matsuda,H., Eletcher,C.F., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Dalla,E., Dragani,T.A., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.D., Kanai,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Nantais,I.H., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Nanchionni,L., McKenzie,L., Miki,H., Nagashima,T., Narchionni,L., Pertea, G., Pertovsky,N., Pillai,R., Pontius,J.U., Oi,D., Ramachanda,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shing,B.Z., Rungwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shing,B.Z., Kangui,T., Wanger,L., Wahlestedt,C., Wang,Y., Waranabe,Y., Wanger,L., Wahlestedt,C., Wang,Y., Waranabe,Y., Hayatsu,M., Hirozane-Kishikawa,T., Yang,J., Narawa,T., Pukuda,S., Hara,A., Hashizume,M., Nakawa,T., Ruckan,J., Nakawa,T., Rakai,M., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,T., Ruda,S., Hara,A., Hashizume,W., Imotani,R., Indotani,R., Rogers,J., Birney,B. and Hayashizaki,Y., Rahailashi,X., Sasaki,D., Shibata,M., Rahailashi,A., Sasaki,D., Sabaski,D., Shibata, A., Naturey,B. and Hayashizaki,Y., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          br/23851 RIKEN full-length enriched, osteoclast-like cell Mus muscaulus cDNA clone 1420020NO5 5', mRNA sequence.
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Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Pax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizawai,K., Akimura,T., Arakawa,T., Carninci,P.,
Adachi,J., Aizawai,R., Akimura,T., Arakawa,T., Carninci,P.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                      GTGAACAGGTTGAGAAGAACAAGATCAACAACAGGGCATCGGAAGAGGCTTTTGTGAAAG
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/mol_type="mRNA"
/db_tref="taxon:10090"
/clone="IMAE:14009081"
/clone="twagE:14009081"
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/lab_host="Dulus"
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/clone lib="Soares mammary gland NMLMG"
/clone lib="soares mammary gland gland"
/clone lib="soares mammary gland with a modified
/clone lib="soares mammary gland with a modified
polylinker; lst strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT713 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."
                 502 bp mRNA linear EST 09-MAR-1999 uc45h03.x1 Soares mammary gland NMLMG Mus musculus cDNA clone IMAGE:1400981 3' Similar to gb:M20469 CLATHRIN LIGHT CHAIN B (HTWAN);, mRNA sequence. A1463714
A1463714. GI:4317744
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tunor Gene Index
Unpublished (1997)
Contact: Robert Stausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LiNL; contact the IndGE Consortium (info@image.llnl.gov) for further information.
MGI:912697
This clone was previously sequenced on the 5' end only, this new data is from the 3' end
Possible reversed clone: polyT not found
High quality sequence stop: 478.
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BE854705 569 bp mRNA linear EST 27-SEP-2000 ux32h10.yl Soares NWMAX maxillary process Mus musculus cDNA clone IMAGE:3512035 5' similar to SW:CLCB_RAT P08082 CLATHRIN LIGHT CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACCTGCCGCCAGCCAGGTGGCCTCTGCGCAGCCCGGACTCGCGAGCGGGGGTGGTTCGG 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 569)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Other ESTS: ux32h10.x1
Other ESTS: ux32h10.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 GCTACGCTGCGATTGCCCAGGCGGACAGGTTGACTCAGGAGCCTGAGAGCATCCGCAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Possible reversed clone: similarity on wrong strand Seq primer: -40RP from Gibco High quality sequence stop: 300. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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   481 ACCCTAAGAGCAGCAAGCAATGTAAAGACGTGTCCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="IMAGE:3512035"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                      GI:10313317
                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
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Unpublished (1997)
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                                                                                                              Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subbraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for trapper-selected cDNAs to prepare Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepare mouse tissues.
Tissues were provided by Takashi Ishikawa ( Department of Surgery Tissues were provided by Takashi Ishikawa ( Vokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama 236-0004 Japan ) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 TCGGGGCACCTGCCGCCAGCCAGGTGGCCTCTGCGCAGCCGGGACTCGCGAGCGGGGCTG 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360
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Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="osteoclast-like cell"
/clone_lib="RIKEN full-length enriched, osteoclast-like
cell"
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Pred. No. 1.8e-105;
0; Mismatches 26;
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1420020N05"
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                       Matches 477; Conservative
  Best Local Similarity
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lochar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Conter
Clone distribution: NG-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF227172 496 bp mRNA linear EST 29-DEC-2000 uz20f03.x1 NCI CGAP Mam5 Mus musculus cDNA clone IMAGE:3669629 3' similar to SW:CLCE_RAT P08082 CLATHRIN LIGHT CHAIN B ;, mRNA
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NCI-CARP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                      86
                                    205 AGGTTGAGAAGAACAAGATCAACAACAGGGCATCGGAAGAGGCTTTTGTGAAAGAATCCA
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Possible reversed clone: similarity on wrong strand High quality sequence stop: 448.
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Length 496;

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87.4%; Score 467.4;

Query Match

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EST213394 Normalized rat heart, Bento Soares Rattus sp. cDNA clone RHEBS34 3' end, mRNA sequence.
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1 ( bases 1 to 476)
1ee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
Rerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
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                                                                      3 CGCCGCCTTCCTGGCCCAGCAGAAAGCGAGATTGCTGGCATCGAGAATGACCCGGGTT
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Other ESTB: FC52991
Contact: Lee. NH
The Institute for Genomic Research
9712. Medical Center Drive, Rockville, MD 20850, USA
FIL: (301)-838-3529
Fax: (301)-838-0208
  Indels
  17;
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                                               cch 87.3%; Score 467.2; DB 1; Length 476; al Similarity 99.4%; Pred. No. 2.3e-104; 469; Conservative 0; Mismatches 3; Indels 0;
                                                Query Match
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Matches 469,
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Search completed: January 5, 2006, 21:32:34 Job time : 3756 secs

Sequence

Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 12583, A Sequence 12583, A Sequence 12583, A Sequence 12197, A Sequence 13192, A Sequence 13192, A Sequence 13192, A

US-09-298-568-1 US-09-410-399-1 US-09-410-399-1 US-08-770-379-2 US-08-770-379-20 US-08-770-378-20 US-09-230-371A-20 US-09-949-016-12583 US-09-949-016-17392 US-09-949-016-17392 US-09-949-016-17361 US-09-949-016-17361 US-09-949-016-17361 US-09-949-016-17361 US-09-949-016-17361 US-09-949-016-17361 US-09-949-016-17361 US-09-130-114-2 US-09-130-114-2 US-09-244-796-17

Sequence 16477, A Sequence 4, Appli Sequence 2, Appli

Sequence 3 Sequence 3 Sequence 3

ALIGNMENTS

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFCATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE:
APPLICATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30,768
REGISTRATION NUMBER: 30,768
REGISTRATION NUMBER: 30,768
REGISTRATION NUMBER: 30,768
REGISTRATION NUMBER: 30,768
REFERENCE/DOCKET NUMBER: 30,72/114 IMMU
TELEPHONE: (703)83-4109
TELEFAX: (703)83-4109
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Sequence 14, Application US/08232463

Patent No. 5670367

GENERAL INFORMATION:
APPLICANT: DORNER:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
MUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER: FOLEY & LATGHEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEB: Foley & Lardner STREET: 1800 Diagonal Road, Suite CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Plan PC Compatible
OPERATING SYSTEM: PC-DOS/MS_DOS
                         CLONE: pTZgpt-Fla
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Sequence 48, Appl
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Sequence 2,
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
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US-09-949-016-1675-

US-09-618-166-209

US-08-781-891-208

US-09-618-166-208

US-09-618-166-208

US-09-618-166-208

US-09-410-389-3

US-09-410-399-3

US-09-130-114-1

US-09-130-114-1

US-09-130-14-1

US-09-130-14-1

US-08-191-15-1

US-08-191-15-1

US-08-91-15-1

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US-09-471-669A-48
US-09-949-016-13042
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Maximum Match 100%
Listing first 45 summaries
                                                                              nucleic search, using sw model
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                                                                                                                                                                      US-10-664-705-145
535
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Maximum DB seq length: 2000000000
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Match Length
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                                                                                 OM nucleic
                                                                                                                                                                                                         Sequence:
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Perfect
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                                                                                                      78 AGCCAGGTGGCCTCTGCGCAGCCCGGACTCGCGAGCGGGGGTTCGGAGGACATGGGG 137
                                                                                                                                                                            138 ACTACAGTCAATGGAGATGTGTTTCAGGAGGCTAACGGGCCTGCCGATGGCTACGCTGCG 197
                                                                                                                                                                                                                                               198 ATTGCCCAGGCGGACAGGTTGACTCAGGAGCCTGAGAGCATCCGCAAGTGGAGAGAGGAG 257
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APPLICANT: ENDEGE, WILSON O., ET AL.
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT APPLICATION NUMBER: 09/328,111
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1998-01-27
EARLIER FILING DATE: 1998-01-37
EARLIER FILING DATE: 1998-01-37
EARLIER FILING DATE: 1998-01-37
SOFTWARE: FREESEQ FOR WINDOWS VERSION 3.0
                             ch 14.6%; Score 78; DB 2; Length 7218; 1 Similarity 5.7%; Pred. No. 3.9e-11; 24; Conservative 245; Mismatches 155; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 327, Application US/09385982 Patent No. 6262334

// LOCATION: (1)...(658)
// OTHER INFORMATION: n = A,T,C or G
US-09-385-982-327

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                                                  Best Local Similarity
Matches 24; Conserv
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US-08-232-463-14
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FALCHANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-09

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16775
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10.4%; Score 55.8; DB 3; Length 1;
Best Local Similarity 53.4%; Pred. No. 5e-05;
Matches 117; Conservative 0; Mismatches 102; Indels
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APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, Junko
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9496 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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STREET:
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Mulligan, John T.
Schellenberg, Gerald D.
SCHELLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
WERNER'S SYNDROME
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Pred. No. 0.00022;
0; Mismatches 113; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                 STREET (2000 Columbia Center, /ur filt.
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COUNTRY: USA
ZIP: 98104-7092
COUNTRY: READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin NATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REGISTRATION NUMBER: 39,317
REPERPORS/COCKET NUMBER: 3
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
SED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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Patent No. 6583112
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
Yu, Chang-En
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Best Local Similarity 51.9%;
Matches 122; Conservative
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US-08-781-891-209
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296 GGTGACCGAACAGGAGTGGCGGGAGAGAGCCAAAAAAGACCTGGAGGAGTGGAACCAGCG 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.1%; Score 54.2; DB 3; Length 51259; Best Local Similarity 51.9%; Pred. No. 0.00022; Matches 122; Conservative 0; Mismatches 113; Indels 0;
COMPUTER REALIST FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Ins PC compatible
COMPUTER: Talm PC compatible
COMPUTER: Talm PC compatible
COMPUTER: Talm PC compatible
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/618,166
FILING DATE: 17-Jul-2000
CILLASSIFICATION: CUBRCOMPA
ATTORNEY/AGENT INFORMATION:
NAME: MACHASTER DATIG D.
REGISTRATION NUMBER: 33,963
REPERRUCE/DOCKET WUMBER: 240052.419C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junn T.
APPLICANT: Schellenberg, Gerald D.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: GENE AND GENE PRODUCTS NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 209:
US-09-618-166-209
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Patent No. 6090620
                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
LENGTH: 51259 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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Sequence 2, Application US/09249585A
Sequence 2, Application US/09249585A
Sequence 2, Application US/09249585A
GENERAL INFORMATION:
APPLICANT: HOTICK, Robert
TITLE OF INVERTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/0D905
CURRENT APPLICATION UNMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOCTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 1926
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 52.8; DB 3; Length 1
Pred. No. 0.00036;
0; Mismatches 157; Indels
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Pred. No. 0.00068;
0; Mismatches 179;
                                                                               NAME: MCMASTERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.419C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1)..(1926)
; OTHER INFORMATION: coding strand of EBNA-1
US-09-249-585A-2
                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 208:
APPLICATION NUMBER: US/09,
FILING DATE: 17-Jul-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                  ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 48.4%;
Matches 147; Conservative
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Best Local Similarity 46.9
Matches 158; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      9.9%; Score 52.8; DB 3; Length 16442;
llarity 48.4%; Pred. No. 0.00036;
Conservative 0; Mismatches 157; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                           ATTORNEY AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAC: (206) 682-6031
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Fu, Ying-Hui
Yu, Chang-En
Oahima, Junko
Mulligan, John T.
Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRO
    US/08/781,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 208, Application US/09618166
Patent No. 6583112
GENERAL INFORMATION:
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                        27-DEC-1996
N: 800
                                                                                                                                                                                                                                                          LENGTH: 16442 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: Washington
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    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-08-781-891-208
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147; Conserv
                        FILING DATE: 2.
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US-09-618-166-208/c
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Matches
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Matches 158;
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Betent No. 6482587

GENERAL INFORMATION:
APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA TITLE OF INVENTION: CHORD DNA TITLE OF INVENTION: LO Genomic Host DNA TITLE OF INVENTION WINDERS: US/09/410,399
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1926
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9.5%; Score 50.6; DB 3;
Best Local Similarity 46.9%; Pred. No. 0.00068;
Matches 158; Conservative 0; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Epstein-Barr virus US-09-410-399-3
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Sequence 2, Application US/09050863
Patent No. 6114111
GENERAL INPORMATION:
APPLICANT: Lao, Ying
APPLICANT: Hao, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: System
TITLE OF INVENTION: System
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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Pred. No. 0.00075;
0; Mismatches 179; Indels
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STREET: 4 Embarcadero Center, Suite 3400
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,863
FILING DATE: 30-MAR-1998
CLASSIFICATION:
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NAME: $11va, Robin M.
REGISTRATION NUMBER: 38,304
REPERENCE/DOCKET NUMBER: A-65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 791-1989
TELEFRY: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                   Hiang, Betty
Payan, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
System
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/050,863
FILING DATE: «Unknown»
ATTORNEY! AGENT INFORMATION:
NAME: $1/00. Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
TELEPONE: (415) 791-1989
ITELEPAN: (415) 791-1989
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGGAGGACCCCAGGCACAGAGTGGGAGAAGGTG 461
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,081
FILING DATE: 22-011-1999
CLASSIFICATION: <UNKNOWN>
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STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
                                                                            Sequence 2, Application US/09359081
Patent No. 6316223
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                        APPLICANT: Lao, Ying
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RESULT 11
US-09-359-081-2
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365 ACAGGTTGAGAAGAACAAGATCAACAACAGGGCATCGGAAGAGGCTTTTGTGAAAGAATC 424
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APPLICANT: Sobbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
TITLE OF INVENTION: Erom Multiple Transfected Episomes
TITLE OF INVENTION: Prom Multiple Transfected Episomes
TITLE OF INVENTION: Prom Multiple Transfected Episomes
CURRENT APPLICATION: NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
9.5%; Score 50.6; DB 2; Length 5
Best Local Similarity 46.9%; Pred. No. 0.00097;
Matches 158; Conservative 0; Mismatches 179; Indels
1197 GGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1233
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S-09-647-344A-14/C

Sequence 14, Application US/09647344A

Patent No. 6586180

GENERAL INFORMATION:

APPLICANT: Ruffner, Duane E.

APPLICANT: Pierce, Michael L.

CURRENT FILICANTON UNDERR: US/09/647,344A

CURRENT APPLICATION NUMBER: PCT/US99/06742

PRIOR FILING DATE: 1999-03-28

NUMBER OF SEQ ID NOS: 50

SEQ ID NO 14

LENGTH: 8705
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US-09-130-114-1/c
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US-09-620-925-1
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                         Query Match
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                                                                                                                                   Score 50.6; DB 3; Length 8705; Pred. No. 0.0011;
                                                                                                                                                                                                     0; Mismatches 179; Indels
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APPLICATION NUMBER: US/08/910,647
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Polymucleotide Delivery
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1218.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08910647
Patent No. 6251433
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STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTYY: U.S.A.
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                   Query Match
Best Local Similarity 46.9%;
Matches 158; Conservative (
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9600 base pairs
                     ; OTHER INFORMATION: pShuttle US-09-647-344A-14
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STRANDEDNESS: single
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US-08-910-647-1
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FEATURE:
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                                                                                                                                                                                   185 TGGCTACGCTGCGATTGCCCAGGCGGACAGGTTGACTCAGGAGCCTGAGAGCATCCGCAA
                                                                                           125 GGAGGACATGGGGACTACAGTCAATGGAGATGTTTTCAGGAGGCTAACGGGCCTGCCGA
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Length 9600;
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CORRESPONDERS ADDRESSE:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Beneryville
STATE: California
CONTRY: U.S.A.
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09620925
Sequence 1, Application US/09620925
Patent No. 6468986
GENERAL INFORMATION:
APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Compositions and Methods for PITLE OF INVENTION: Polynucleotide Delivery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425 CAAGGAGGAGCCCCAGGCACAGAGTGGGAGAAGGTG 461
    Score 50.6; DB 3; 1
Pred. No. 0.0012;
0; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/620,925
FILING DATE: 21-Jul-2000
CLASSIPICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION WOMBER: 08/910,647
FILING DATE: «UNKnOWN»

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 12:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
TELEPHONE: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 9600 base pairs
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STRANDEDNESS: single
    9.5%;
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                                                    Matches 158; Conservative
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                                                                                         125 GGAGGACATGGGGACTACAGTCAATGGAGATGTTTTCAGGAGGCTAACGGGCCTGCCGA 184
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                                                                                                                          185 TGGCTACGCTGCGATTGCCCAGGCGGACAGGTTGACTCAGGAGCCTGAGAGCATCCGCAA 244
                                                                                                                                                                           245 GTGGAGAGGAGGAGAAAAAAGGCTGCAGGAGTTGGATGCTGCCTCGAAGGTGACCGA 304
                     Query Match 9.5%; Score 50.6; DB 3; Length 9600; Best Local Similarity 46.9%; Pred. No. 0.0012; Matches 158; Conservative 0; Mismatches 179; Indels 0; Gaps
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Search completed: January 5, 2006, 21:35:23 Job time : 162 secs

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Sequence 2289, Ap
Sequence 28203, A
Sequence 11137, A
Sequence 11137, A
Sequence 29408, A
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3009, Ap
8244, Ap
1303, Ap
213, App
178, App
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26855, A
27337, A
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265, App
2036, Ap
14, Appl
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Sequence 1407, Ap
                                                                                    January 5, 2006, 19:33:09 ; Search time 804 Seconds (without alignments) 5502.633 Million cell updates/sec
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1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
6: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
7: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
8: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
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10: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-191-803-255
US-10-191-803-265
US-10-439-703-14
US-10-956-157-3009
US-10-956-157-3009
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US-10-242-535A-29408
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US-09-918-995-28203
                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                 9793542 seqs, 4134689005 residues
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Sequence 10148, A Sequence 11648, A Sequence 116616, Sequence 116616, Sequence 24924, A Sequence 20524, A Sequence 20525, A Sequence 26043, A Sequence 24460, A Sequence 24460, A Sequence 210020, A Sequence 210020, A Sequence 210020, A Sequence 228043, A Sequence 228043, A Sequence 228043, A Sequence 228043, A Sequence 210020, A Sequence 228043, A Sequence 22804,
US-10-085-783A-29408 US-09-918-995-10148 US-09-925-065A-555818 US-10-424-599-116616 US-09-925-065A-899680 US-10-242-515A-24924 US-10-085-783A-24924 US-10-097-143-41371 US-10-097-143-41371 US-09-918-995-20559 US-10-097-143-41371 US-09-918-995-20659 US-10-242-515A-24460 US-10-242-515A-24460 US-10-242-515A-24460 US-10-246-515A-24460 US-10-246-615-71 US-09-871-161-327 US-10-972-079-49308 US-10-972-079-49308 US-10-097-143-21013 US-10-097-143-21013
419 473 489 489 489 476 476 3201 481 1764 461 461 411 658 622 622 639 629 629 639 629
222 222 222 201 110 110 110 110 110 110
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## ALIGNMENTS

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Sequence 145. Application US/10664705

Sequence 145. Application WS/10664705

Publication No. US20040152107A1

GENERAL INFORMATION

APPLICANT: Alter, Anthony C.

APPLICANT: Alter, Anthony C.

APPLICANT: Charles A.

APPLICANT: Withman, Yury

APPLICANT: Bukhman, Wury

APPLICANT: 03236/1000087-US2

CURRENT FILING DATE: 2002-09-18

PRIOR FILING DATE: 2002-12-09

PRIOR FILING DATE: 2002-12-09

PRIOR FILING DATE: 2003-61-8

PRIOR FILING DATE: 2003-61-8

SEQUENARE: PatentIn version 3.1

SEQUENARE: PatentIn version 3.1
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100.0%; Score 535; DB 7; L
Best Local Similarity 100.0%; Pred. No. 1.2e-144;
Matches 535; Conservative 0; Mismatches 0;
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; ORGANISM: Rattus norvegicus
US-10-664-705-145
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99 CGGCCGCCTTCCTGGCCCAGCAGAGAGCGAGATTGCTGGCATCGAGAATGACTCGGGTT 158
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APPLICANT: Suter-Dick, Laura
APPLICANT: Ster-Dick, Laura
APPLICANT: Wolf, Detlef,
TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
TITLE REPERENCE: 21199
CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
PRIOR PILING DATE: 2002-03-14
PRIOR PLILING DATE: 2002-03-14
PRIOR PILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
SOFTWARKE: Patentin version 3.1
SEQ ID NO 227
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Pred. No. 4.7e-126;
0; Mismatches 0; Indels
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US-10-388-934-227
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Best Local Similarity 90.8%;
Matches 535; Conservative (
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GCAAGTGGAGAGGAGCAGAAGAAAAGGCTGCAGGAGTTGGATGCTGCCTCGAAGGTGA
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US-09-917-800A-1407
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APPLICANT: PORTECT, MARK
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REPREBUCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-11-02
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-12
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-22
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-19
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Best Local Similarity 90.8%; Pred. No. 4.7e-126;
Matches 535; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1407, Application US/09917800A Patent No. US20020119462A1
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1407
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US-09-917-800A-1407
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                                          579 AGGAGGAGACCCCAGGCACAGAGTGGGAGAAGGTGGCCCAGCTGTGTGACTTCAACCCTA
159 TCGGGGCACCTGCCGCCAGCCAGGTGGCCTCTGCGCAGCCGGACTCGCGAGCGGGGTG
                           GTTCGGAGGACATGGGGGACTACAGTCAATGGAGATGTGTTTCAGGAGGCTAACGGGCCTG
                                                                                 CCGATGGCTACGCTGCGATTGCCCCAGGCGGACAGGTTGACTCAGGAGCCTGAGAGCATCC
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APPLICANT: PORTER, Mark

APPLICANT: PORTER, Mark

APPLICANT: JOHNSON, KGTY

APPLICANT: GASTLE, Arthur

APPLICANT: CASTLE, Arthur

APPLICANT: ELASHOFP, Michael

TITLE OF INVENTION: Cardiocoxin Molecular Toxicology Modeling

FILE REFERENCE: 44921-5090US

CURRENT APPLICATION NUMBER: US/10/191,803

CURRENT FILING DATE: 2001-07-10

PRIOR PILING DATE: 2001-07-10

PRIOR FILING DATE: 2001-07-17

PRIOR FILING DATE: 2001-07-17

PRIOR FILING DATE: 2002-04-03

PRIOR FILING DATE: 2002-04-03

PRIOR FILING DATE: 2002-05-06

NUMBER OF SEQ ID NOS: 1140

SOFTWARE: PALENTIN VENCE: 211

SEQ ID NO 265

LENGTH: 982
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90.8%; Pred. No. 4.7e-126;
:ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 265, Application US/10191803
Publication No. US20040014040A1
GENERAL INFORMATION:
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PEATURE:
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Matches 535; Conserva
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CCGATGGCTACGCTGCGATTGCCCAGGCGGACAGGTTGACTCAGGAGCCTGAGAGCATCC
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APPLICANT: Johnson, Kory
APPLICANT: Higgs, Brandon
APPLICANT: Elsable, Arthur
Elsable, Arthur
Elsable, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR PILING DATE: 2001-06-13
PRIOR PILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-19
PRIOR PILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR PILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,808
PRIOR PILING DATE: 2001-09-28
PRIOR PILING DATE: 2001-09-28
PRIOR PILING DATE: 2001-09-27
PRIOR PILING DATE: 2001-09-27
PRIOR PILING DATE: 2001-11-01
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APPLICANT: Williams, Amanda
APPLICANT: Boland, Joseph F.
APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Averal, Jon C.
APPLICANT: Wetzel, Jon C.
APPLICANT: Wockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
FILE REFERENCE: 4921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT PILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US 60/193,446
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: PatentIN Ver. 2.1
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                                                                                                                                Length 1051;
                                                                                                                                                                    Indels
                                                                                                                              Score 451.8; DB 7;
Pred. No. 1.7e-120;
0; Mismatches 52;
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                                                                                                                                 84.4%;
     version 3.1
                                                                                                                                Query Match
Best Local Similarity 90.3
Matches 483; Conservative
   ; SOFTWARE: Patentin v
; SEQ ID NO 14
; LENGTH: 1051
; TYPE: DNA
                                                                            ORGANISM: Human
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LENGTH: 1051
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US-10-439-703-14
US-10-439-703-14
Sequence 14, Application US/10439703
Publication No. US20040018527A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPPLICANT: Chang, Jenny
APPLICANT: Chang, Jenny
TITLE OF INVENTION: Chemosensitivy and Chemoresistance
TITLE OF INVENTION: Chemosensitivy and Chemoresistance
TITLE OF INVENTION: Chemosensitivy and Chemoresistance
TITLE OF INVENTION UNDER: US/10/205813
CURRENT APPLICATION NUMBER: US/10/439,703
CURRENT APPLICATION NUMBER: US/60/381,141
PRIOR FILING DATE: 2002-05-17
NUMBER OF SEQ ID NOS: 91
                                                                                                                                                                                                                                                                                                                                      99 CGGCCGCCTTCCTGGCCCAGCAGGAGCGAGATTGCTGCAGAATGATCGAGAATGACTCGGGTT 158
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PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILING DATE: 2001-10-22
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ. 10 NOS: 2.221
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2036
LENGTH: 982
                                                                                                                                                                                                                                                                                 54;
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                                                                                                                                                                                     ; OTHER INFORMATION: Genbank Accession No. NM_053835
US-10-152-319A-2036
                                                                                                                                                                                                                                         88.0%; Score 471; DB 7; L. 90.8%; Pred. No. 4.7e-126; cive 0; Mismatches 0;
                                                                                                                                   TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.8
Matches 535; Conservative
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Sequence 8244, Application US/10956157

Sequence 8244, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:
Publication No. US20050118625A1

GENERAL INFORMATION:
APPLICANT: Wyear

TITLE OF INVENTION: HUMAN OSTEOARTHATIS AND HUMAN PROTEASES

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: Patentin version 3.2

SEQ ID NO 8244
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                                                                                                                                                                                              AAAGACCTGGAGGAGTGGAACCAGCGCCAAAGTGAACAGGTTGAGAAGAACAAGATCAAC 389
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                                                           GGAGATGTGTTTCAGGAGGCTAACGGGCCTGCCGATGGCTACGCTGCGATTGCCCCAGGCG
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89.5%; Pred. No. 1.2e-108;
iive 0; Mismatches 52;
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Matches 453; Conservative
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CORGANISM: Homo sapiens
US-10-956-157-8244
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US-10-956-157-3009

US-10-956-157-3009

US-10-956-157-3009

Subjection US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wyeth

TILE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

TILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

FILE REPERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 318905

SOFTWARE: PATENTIN version 3.2
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            ; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 M20470
US-10-240-425-1304
                                                                  Length 1051;
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                                                                  Score 451.8; DB 7;
Pred. No. 1.7e-120;
0; Mismatches 52;
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Pred. No. 1.2e-108;
0; Mismatches 52;
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Best Local Similarity 89.5%;
Matches 453; Conservative
                                                                     Query Match
Best Local Similarity 90.3%;
Matches 483; Conservative
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CRCANISM: Homo sapiens
US-10-956-157-3009
ORGANISM: Homo sapiens
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; Sequence 213, Application US/09823245A
; Publication No. US20020039760A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Agostino, Michael J.
; APPLICANT: Agostino, Michael J.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Genetick, Ramalakar
; APPLICANT: Graham, James R.
; APPL
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US-09-823-245A-213
                                                                                                                                                                301
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; Publication No. US2040033502A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Alvarez, Chris
; APPLICANT: Scherf, Uwe
; APPLICANT: Wockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; PILE REFERENCE: 44921-5026
; CURRENT PILING DATE: 2002-09-30
; FILE REPERIOR UNMBER: DCT/US01/09847
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR APPLICATION NUMBER: US 60/193,446
; RIUNG BATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; FENDING 1303
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US-10-240-425-1303
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ORGANISM: Homo sapiens
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667 GCGAGAGGAGCAGAGGAAACGCTGCAAGAGCTGCATCTAAGGTCACGAACA
                                                                                                                                                                                                                                                                                               434 GACCCCAGGCACAGAGTGGGAGAGAGGTGGCCAGCTGTGACTTCAACCCTAAGAGCAG
                                                                                                              GGAGTGGCGGAGAGGGCCAAAAAAAGACCTGGAGGAGTGGAACCAGCGCCAAAGTGAACA
                                                                                                                                                   ------GGCATCGGAAGAGCTTTTGTGAAAGAATCCAAGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 CAAGCAGTGCAAAGATGTGTCCCGCCTGCGGCTCGGTGCTCAT 326
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                                                                                                                                                                                                                                                              368 GGTTGAGAAGAACAAGATCAACAACAG-----
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US-09-918-995-20102
US-09-918-995-20102, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFERMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , LOCATION: (1) ... (490)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-20102
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Best Local Similarity 89.3<sup>3</sup>
Matches 392; Conservative
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LOCATION: (1)...(490)
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                534 AGTAGAGAAGAAGAAGAACAACAACAGATCGCTGACAAAGGCATTCTACCAGCAGCCAGA 475
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US-09-823-245A-178/C

Sequence 178, Application US/09823245A

Publication No. US20020039760A1

GENERAL INFORMATION

APPLICANT: Word, Gordon G.

APPLICANT: Pechtel, Kim

APPLICANT: Reshick, Hilary

APPLICANT: Reshick, Richard J.

APPLICANT: Reshick, Richard J.

APPLICANT: Graham, James R.

APPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 70.9%; Score 379.2; DB 3; Best Local Similarity 81.6%; Pred. No. 1.7e-99; Matches 475; Conservative 0; Mismatches 53;
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ORGANISM: Homo sapiens
US-09-823-245A-178
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                                                                                                                                                             RESULT 14
US-09-2918-995-26855
US-09-2018-995-26855
Sequence 26855, Application US/09918995
Fublication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PAPLICATION NUMBER: US/09/235,076
PRIOR PLICATION NUMBER: US/09/235,076
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26855
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc_feature
; LOCATION: (1)...(493)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-26855
                                                                                                         464 GCCTGGCTCGGTGCTCAT 482
                                                                                             GCCTGCGCTCGGTGCTCAT 535
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ORGANISM: Homo sapiens
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         Sequence 2737, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INPORMATION:
; TITLE OF INVENTION:
; TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
; TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
; TITLE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: PSESEQ for Windows Version 3.0
; SEQ ID NO 27337
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; LOCATION: (1)...(485)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-27337
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Job time : 807 secs
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                                                                    ; Search time 312 Seconds (without alignments) 1249.941 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-955-054A-123
US-11-121-086-24
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US-11-122-908-19
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Maximum Match 100%
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US-10-995-561-13220 US-11-136-527-2555 US-11-136-527-4371 US-11-136-527-4371 US-11-136-527-4371 US-11-136-527-3217 US-10-995-561-21286 US-10-995-561-147 US-10-995-561-146 US-10-995-561-144 US-10-995-561-144 US-10-995-561-145 US-11-121-086-106 US-11-121-086-106 US-11-121-086-106 US-11-121-086-106 US-11-121-086-106 US-11-121-086-106 US-11-121-086-106 US-11-121-086-106 US-11-121-086-106 US-11-121-086-106 US-11-121-086-106 US-11-121-086-106 US-11-121-086-106	US-10-995-561-499 US-10-995-561-498
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## ALIGNMENTS

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        Sequence 1696, Application US/11136527
Sequence 1696, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REPERENCE: 031896-041000 (AMA101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-26
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1696
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                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA; Rattus norvegicus US-11-136-527-1696
US-11-136-527-1696
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US-10-955-054A-94
Sequence 94, Application US/10955054A
; Bequencion No. US20050266420A1
                                                                                     ; Sequence 589, Application US/10821234; Publication No. US20050255114A1; GENERAL INFORMATION:
              Query Match
Best Local Similarity 63.7%;
Matches 341; Conservative 0
                                                                                                                                                                                                                                                                                                        TYPE: DNA
CORGANISM: Homo sapiens
US-10-821-234-589
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Sequenct 5792, Application US/11136527
; Bublication No. US20850287570A1
; GENERAL INFORMATION:
APPCICANT: Wyeth
APPCICANT: Woth
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT FILING DATE: 2005-05-05-05
FRIOR APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-05-05
; RIOR FILING DATE: 2005-05-05
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5792
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; Pred. No. 6.5e-118;
51; Mismatches 0;
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; ORGANISM: Rattus norvegicus
US-11-136-527-5792
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Best Local Similarity 89.8'
Matches 451; Conservative
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APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Adammani, Susan
APPLICANT: Andarmani, Susan
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REPERBERS: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
FURN APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SEQ ID NOS: 1704
SEQ ID NO 589
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Pred. No. 3.6e-47;
0; Mismatches 191;
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APPLICANT: Wounts, William M
APPLICANT: Wounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE REFERENCE: 071896-041000 (AM.01086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT APPLICATION NUMBER: US 60/574,294
PRIOR PILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
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                     APPLICANT: PUSZTAI, LAJOS
APPLICANT: SYMANS, W. FRASER
APPLICANT: SYMANS, W. FRASER
APPLICANT: HESS, KENNETH R.
APPLICANT: AYERS, MARK
APPLICANT: AYERS, MARK
APPLICANT: STEC, JAMES
TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
FILE REPERBNCE: UTXC:880US
CURRENT APPLICATION NUMBER: US/10/955,054A
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 94
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Publication No. US20050287570A1
GENERAL INFORMATION:
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Best Local Similarity 63.7%;
Matches 341; Conservative (
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GENERAL INFORMATION:
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Publication No. US20050287570A1
Publication No. US20050287570A1
Publication No. US20050287570A1
APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANTION: Probe Arrays For Expression Profiling of Rat Genes File REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
                                                                                                                                                                                                                                                                                                                   1 CGGCCGCCTTCCTGGCCCAGCAGAGAGATTGCTGGCATCGAGAATGACTCGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                       Length 1169;
                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                    27.3%; Score 146; DB 7; 1
56.8%; Pred. No. 2.5e-29;
tive 14; Mismatches 180;
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SOFTWARE: Patentin version 3.2
SEQ ID NO 4443
SOFTWARE: Patentin version 3.2
SEQ ID NO 347
LENGTH: 1169
                                                                                          ; TYPE: DNA; CREALUS norvegicus US-11-136-527-347
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Matches 259; Conservative
                                                                                                                                                                                                                                        Similarity
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16326 AACAGGAGGAGGA 16338
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Best Local Similarity 48.9
Matches 153; Conservative
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Matches 108; Conservative
                                                                                                                                                                                                              ORGANISM: Homo sapiens
US-11-121-086-5
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                                                                                                                                                                               LENGTH: 153376
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                                                                                                                                                                                                TYPE: DNA
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TCGGGGCACCTGCCGCCAGCCAGGTGGCCTCTGCGCAGCCCGGACTCGCGAGCGGGGGTG 120
                                                              GTTCGGAGGACATGGGGACTACAGTCAATGGAGATGTTGTTTCAGGAGGCTAACGGGCCCTG 180
                                                                                             327 GTCCTGATGCGGTTGATGGAGTGATGAATGGCGAATACTACCAGGAGAGCAATGGTCCAA 386
                                                                                                                                                               387 CAGACAGTTACGCAGCCATTTCAGAAGTGGATCGGTTGCAGTCAGAGCCTGAAAGTATCC 446
                                                                                                                                                                                                GCAAGTGGAGAGAGAGCAGAAAAAAGCTGCAGGAGTTGGATGCTGCCTCGAAGGTGA 300
                                                                                                                                                                                                                                 447 GTAAGTGGAGAGAGAGCAGACAGAGCGCCTGGAAGCCCTCGATGCCAATTCTCGGAAGC 506
                                                                                                                                                                                                                                                                  CCGAACAGGAGTGGCGGGAGAAGGCCAAAAAAGACCTGGAGGAGTGGAACCAGCGCCAAA 360
                                                                                                                                                                                                                                                                                                GTGAACAGGTTGAGAAGAACAAGATCAACAGGGCATCGGAAGAGGCTTTTGTGAAAG 420
                                                                                                                                                                                                                                                                                                                                                    TCGCCATCCTAGACGGCGGC---GCCCCGGGCCGCAGGMACACGCGGGGGGCCCCCGGGGG
                                                                                                                                CCGATGGCTACGCTGCGATTGCCCCAGGCGGACAGGTTGACTCAGGAGCCTGAGAGCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 CAGGGCATCGGAAGAGGCTTTTGTGAAAGAATCCAAGGAGAGACCCCAGGCACAGAGTG
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APPLICANT: SYMANS, W. FRASER
APPLICANT: HESS, KENNETH R.
APPLICANT: HESS, MARK
APPLICANT: AYERS, MARK
APPLICANT: STEC, JAMES
TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
FILE REFERENCE: UTXC:88002
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 123
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Pred. No. 2.3e-14;
0; Mismatches 34; Indels 0
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Matches 110; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
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US-11-121-086-5
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; Sequence 5, Application US/11121086 ; Publication No. US20050266459A1 ; GENERAL INFORMATION:

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Publication No. US20050266459A1

GENERAL INFORMATION:
APPLICANT: NIELSEN, KIRSTEN V.
TILLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILER REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PATENTIN VERSION 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 ATGCTGCCTCGAAGGTGACCGAACAGGAGTGGCGGGAGAAGAGGCCAAAAAAGACCTGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 AGGAGGCTAACGGGCCTGCCGATGGCTACGCTGCGATTGCCCCAGGCGGACAGGTTGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 AGGAGCCTGAGAGCATCCGCAAGTGGAGAGGAGCAGAAGAAAAAAGGCTGCAGGAGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343 AGTGGAACCAGCGCCAAAGTGAACAGGTTGAGAAGAACAACAACAACAACAACAGGGCATCGG
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APPLICANT: NIELSEN, KIRSTEN V.

TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138.600-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04

PRIOR RPPLICATION NUMBER: 60/567,570

PRIOR FILING DATE: 2004-05-04

SOFTWARE: PATENTI NOS: 107

SOFTWARE: PATENTIN VERSION 3.3

SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                                               Length 153376;
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Pred. No. 2.5e-05;
0; Mismatches 160; Indels
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365 ACAGGTTGAGAAGAACAAGATCAACAACAGGGCATCGGAAGAGGCTTTTGTGAAAGAATC 424
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                                                                                                                                                                                                                                                                                                                                                                                                                 249 AGAGAGGAGCAGAAAAAGGCTGCAGGAGTTGGATGCTGCCTCGAAGGTGACCGAACAG
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Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: POULSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US.11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
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Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                 Score 47.8; D)
Pred. No. 0.00'
0; Mismatches
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PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR FILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: US 60/633,826
PRIOR FILING DATE: 2004-12-07
NUMBER OF SEQ ID NOS: 511
SOFTWARE: PATENTIN VEXBION 3.3
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.5%;
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SOFTWARE: PatentIn version 3.3
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Best Local Similarity 57.8%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 45.6
Matches 160; Conservative
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COGANISM: Homo sapiens
US-11-121-086-3
                                                                                                                                                                                                                                   CRGANISM: Homo sapiens US-11-112-908-19
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                                        322
                                        GAAAAGGCTGCAGGAGTTGGATGCTGCCTCGAAGGTGACCGAACAGGAGTGGCGGGAGAA
                                                                                        GGCCAAAAAAGACCTGGAGGAGTGGAACCAGCGCCAAAGTGAACAGGTTGAGAAGAACAA
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8.9%; Score 47.8; DB 7; Length 207908;
Best Local Similarity 57.8%; Pred. No. 0.0072;
Matches 85; Conservative 0; Mismatches 62; Indels 0;
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US-11-198-19
Sequence 19, Application US/11112908
Sequence 19, Application US/11112908
Publication No. US20050260659A1
GENERAL INFORMATION:
TAPPLICANT: HATIS, Cole
APPLICANT: BAYIS, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFRENCE: 04-16-4US
CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/564,758
PRIOR APPLICATION NUMBER: US 60/564,758
PRIOR APPLICATION NUMBER: US 60/56598
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR FILING DATE: 2004-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/11112908

Publication No. US200502605591

GENERAL INFORMATION:

APPLICANT: Harris, Cole

APPLICANT: Bavis, Lisa M.

TITLE OF INVENTION: Breast Cancer Biomarkers

TITLE OF INVENTION: Breast Cancer Biomarkers

FILE REPERENCE: 04-164-02

CURRENT APPLICATION NUMBER: US/11/112,908

CURRENT FILING DATE: 2004-04-23

PRIOR PILING DATE: 2004-04-33

PRIOR PILING DATE: 2004-06-13

PRIOR PILING DATE: 2004-06-10

PRIOR APPLICATION NUMBER: US 60/575,978

PRIOR PILING DATE: 2004-06-10

PRIOR APPLICATION NUMBER: US 60/631,702

PRIOR PILING DATE: 2004-11-30

PRIOR PILING DATE: 2004-11-30
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LENGTH: 207908
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Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William M
TITLE OF INVEWTION: Probe Arrays For Expression Profiling of Rat Genes FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-26
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
                                                                                                                         Sequence 7472, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-25
PRIOR FILING DATE: 2005-05-26
PRIOR FILING DATE: 2005-05-26
SOFTWARE: Patentin version 3.2
SEQ ID NO 7472
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; ORGANISM: Rattus norvegicus
US-11-136-527-7472
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GAGCATCCGCAAGTGGAGAGGAGCAGAAAAAAAGGCTGCAGGAGTTGGATGCTGCCTC 292
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Pred. No. 0.029;
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Job time : 315 secs
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Best Local Similarity 45.6%;
Matches 155; Conservative C
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